

	30	701	15.3	806	1	TVMHUF3	fibroblast growth
Oy	31	698.5	15.3	812	1	A36477	fibroblast growth
	32	697.5	15.3	650	1	JC1450	fibroblast growth
	33	695.5	15.2	802	1	TVC1450	fibroblast growth
	34	686.5	15.0	824	2	S24108	protein-tyrosine k
	35	686	15.0	799	2	S18209	fibroblast growth
	36	683	14.9	821	1	TVMHUF2	fibroblast growth
	37	679	14.9	822	2	I49289	fibroblast growth
	38	677	14.8	822	1	TVMHUF3	fibroblast growth
	39	677	14.8	876	2	I49152	protein-tyrosine k
	40	677	14.8	880	2	B53743	protein-tyrosine k
	41	674.5	14.8	820	2	S17295	fibroblast growth
	42	672	14.7	819	1	TVCHEG	fibroblast growth
	43	671.5	14.7	769	2	S16236	fibroblast growth
	44	671.5	14.7	822	2	A45081	fibroblast growth
	45	670.5	14.7	821	1	TVMSBK	fibroblast growth

ALIGNMENTS

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RESULT      1
148696
Protein-tyrosine kinase (EC 2.7.1.112) nsK2 precursor, splice form 2 - mouse
N:Alternate names: receptor-type tyrosine kinase
N:Contains: protein-tyrosine kinase nsK2 precursor, splice form 4
C:Species: Mus musculus (house mouse)
C:Date: 19-May-2000 #sequence_revise_19-May-2000 #text_change_19-May-2000
A:Accession: I48696; S60738
R:Ganju, P.; Wallis, E.; Brennan, J.; Reith, A.D.
Oncogene 11, 281-290, 1995
A>Title: Cloning and developmental expression of Nsk2, a novel receptor tyrosine kinase
A:Reference number: I48696; MUID:95349951
A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A:Accession: I48696
A:Molecule type: mRNA
A:Residues: 1-871 <GAN1>
A:Cross-references: EMBL:X86444; NID:9929723; PID:NCAA60165.1; PID:9929724
A:Experimental source: splice form 2
A:Accession: S60738
A:Molecule type: DNA
A:Residues: 1-456; 'A',466-871 <GAN2>
A:Cross-references: EMBL:X86444; NID:9929723
A:Experimental source: splice form 4
C:Comment: For alternate splice forms see PTR:I48697.
C:Genetics:
A:Gene: nsk2
A:Cross-references: MGI:103308
C:Superfamily: mouse ror-related receptor; immunoglobulin homology; protein kinase ho
C:Keywords: ATP; glycoprotein; phosphotransferase; receptor; transmembrane protein; t
F:1/21/Domains: signal sequence #status predicted <SIG>
F:22-871/Product: protein-tyrosine kinase nsK2, splice form 2 #status predicted <MA72
F:22-456,'A',466-871/Product: protein-tyrosine kinase nsK2, splice form 4 #status pre
F:42-101/Domains: immunoglobulin homology <IMM1>
F:135-192/Domains: immunoglobulin homology <IMM2>
F:226-284/Domains: immunoglobulin homology <IMM3>
F:498-518/Domains: transmembrane #status predicted <TRM>
F:575-865/Domains: protein kinase homology <TKN>
F:583-591/Region: protein kinase ATP-binding motif
F:222,462/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match          90.5%; Score 4136; DB 1; Length 871;
Best Local Similarity 90.3%; Pred. No. 7.3e-200;
Matches 790; Conservative 30; Mismatches 45; Indels 10; Gaps 4;
Oy      1 MRELVINIPHLIITLVAFSGTEKLPRKAPVTTPLETVDAIVEEATPMCAVESYPOPEIS 60
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1 MRELVINIPLOMLTIVAFSGTEKLPRKPVIATPLETVDAIVEEATPMCAVESYPOPEIS 60
Oy      61 WTRKKILIKLFDRYSIRENGQLTTLVSDDSDGYCTANNVGAVESCGALQVRMK 120
        |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      61 WTRKKILIKLFDRYSIRENGQLTTLVSDDSDGYCTANNVGAVESCGALQVRMK 120

```

QY 121 PKTRPPINVKIIIEGLKAVLPCCTMGNPKPSVSWIKGDSPLRENSRIALVESSLRHNV 180  
 Db 121 PKTRPPINVKIIIEGLKAVLPCCTMGNPKPSVSWIKGDSPLRENSRIALVESSLRHNV 180  
 QY 181 OKEDAGGYRCYAKNSLGTAVSKVYKLEFEVFAIRILRAPESHNVTFGSFVTLHCTATGIPV 240  
 Db 181 OKEDAGGYRCYAKNSLGTAVSKVYKLEFEVFAIRILRAPESHNVTFGSFVTLHCTATGIPV 240  
 QY 241 PTTWIENGNAVSSGSIOESYKDVYDSRLQFLTTRKGLYCIAATNKHGEKFSRKAAT 300  
 Db 241 PTTWIENGNAVSSGSIOESYKDVYDSRLQFLTTRKGLYCIAATNKHGEKFSRKAAT 300  
 QY 301 ISIAEMSKPQDNKGYCAQYRGEVCNAYL-----AKDALVEL-NTSYADPEAOELLVHT 354  
 Db 301 ISIAEMSKQKDSQGYCAQYRGEVCNAYL-----AKDALVEL-NTSYADPEAOELLVHT 357  
 QY 355 AMNELKAVSPVCPRAEALLCNHIFQECSPGVPTPIICREYCLAVKELFCAKEMLYME 414  
 Db 355 AMNELKAVSPVCPRAEALLCNHIFQECSPGVPTPIICREYCLAVKELFCAKEMLYME 417  
 Y 415 EKHRLGLRSEMHLLSVKCKSLPSMHDPTACARLPHLDYKNKELKTFPPMTSSKPSVD 474  
 Db 415 EKHRLGLRSEMHLLSVKCKSLPSMHDPTACARLPHLDYKNKELKTFPPMTSSKPSVD 477  
 QY 475 IPNLPSSSSSSFSPYPTSMVTIISIMSSFAIVLLITTTLYCCRRRQKMKKRESAY 534  
 Db 475 IPNLPSSSSSSFSPYPTSMVTIISIMSSFAIVLLITTTLYCCRRRQKMKKRESAY 536  
 QY 535 TLTTLPSSELLDRHPNMYQRMPLLNPKLLSLEYPNNTIEYVADIGEAGFGRFOARA 594  
 Db 535 TLTTLPSSELLDRHPNMYQRMPLLNPKLLSLEYPNNTIEYVADIGEAGFGRFOARA 596  
 QY 595 PGLLPYEPFTWAVAKMLEEASADQADFOREAALMAFNDPNYIKLLGVCAYGKPMCLL 654  
 Db 595 PGLLPYEPFTWAVAKMLEEASADQADFOREAALMAFNDPNYIKLLGVCAYGKPMCLL 656  
 QY 655 FEYMAVGDNLNEFLRSMSPHTVCSLSHSDLSMPAOVSSGPPPLSCAEQLCIARQVAAAMA 714  
 Db 655 FEYMAVGDNLNEFLRSMSPHTVCSLSHSDLSMPAOVSSGPPPLSCAEQLCIARQVAAAMA 716  
 QY 715 YLSEKKEFHRDLATRNCLVGNMNVKLTADFGLSRNTYSADYKKAENAIPIRMMPPESI 774  
 Db 715 YLSEKKEFHRDLATRNCLVGNMNVKLTADFGLSRNTYSADYKKAENAIPIRMMPPESI 776  
 QY 775 FYNRTTESDWAYGVVLMEIFSYGLQPYGYGMAHEVITYYVADGNILSCPENCPVELYNL 834  
 Db 775 FYNRTTESDWAYGVVLMEIFSYGLQPYGYGMAHEVITYYVADGNILSCPENCPVELYNL 836  
 QY 835 MRLCKSLPADRPSTSIHRIILERMKCEAEGTAVY 869  
 Db 835 MRLCKSLPADRPSTSIHRIILERMKCEAEGTAVY 871  
 Db 837 MRLCKSLPADRPSTSIHRIILERMKCEAEGTAVY 871

RESULT 2  
 148697 protein-tyrosine kinase (EC 2.7.1.112) nsk2 precursor, splice form 1 - mouse  
 N:Alternate names: receptor-type tyrosine kinase  
 C:Contains: protein-tyrosine kinase nsk2 precursor, splice form 3  
 C:Species: Mus musculus (house mouse)  
 C>Date: 19-May-2000 #sequence\_revision 19-May-2000 #text\_change 19-May-2000  
 C:Accession: 148697; S60740  
 R:Ganju, P.; Walls, E.; Brennan, J.; Reith, A.D.  
 A:Title: Cloning and developmental expression of Nsk2, a novel receptor tyrosine kinase  
 A:Reference number: 148696; MUID:95349551  
 A:Accession: 148697  
 A:Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-881 <GAN1>  
 A:Cross-references: EMBL:X86445; NID:g929725; PID:CA60166.1; PID:g929726  
 A:Experimental source: splice form 1  
 A:Accession: S60740

A:Molecule type: DNA  
 A:Residues: 1-456, 'A', 466-881 <GAN2>  
 A:Cross-references: EMBL:X86445; NID:g929725  
 A:Experimental source: splice form 3  
 C:Comment: For alternate splice forms see PIR:148696.  
 C:Genetics:  
 A:Gene: nsk2  
 A:Cross-references: MGI:103308  
 C:Superfamily: mouse ror-related receptor; immunoglobulin homology; protein kinase ho  
 C:Keywords: ATP; glycoprotein; phosphotransferase; receptor; transmembrane protein; t  
 F:1-21/Domain: signal sequence #status predicted <Sig>  
 F:22-881/Product: protein-tyrosine kinase nsk2, splice form 1 #status predicted <Mat1  
 F:22-456, 'A', 466-881/Product: protein-tyrosine kinase nsk2, splice form 3 #status pre  
 F:42-101/Domain: immunoglobulin homology <IMM1>  
 F:135-192/Domain: immunoglobulin homology <IMM2>  
 F:226-284/Domain: immunoglobulin homology <IMM3>  
 F:498-518/Domain: transmembrane #status predicted <TRM>  
 F:575-865/Domain: protein kinase homology <Kin>  
 F:583-591/Region: protein kinase ATP-binding motif  
 F:222,462/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 90.3% Score 4128; DB 1; Length 881;  
 Best Local Similarity 90.4%; Pred. No. 1,9e-199;  
 Matches 786; Conservative 30; Mismatches 44; Indels 10; Gaps 4;

QY 1 MRELVINPLVHLLTVAESGTEKLPKAVITTPLETVDALVEVATFCAVESYPOPEIS 60  
 Db 1 MRELVINPLQMLTLVARSGETEKLPPVVIATPLETVDALVEVATFCAVESYPOPEIS 60  
 QY 61 WTRNKILKLDTRKSTENQQLTILSVEDSDGTYCCANNVGVGAVESGALQVYMK 120  
 Db 61 WTRNKILKLDTRKSTENQQLTILSVEDSDGTYCCANNVGVGAVESGALQVYMK 120  
 QY 121 PKTRPPINVKIIIEGLKAVLPCCTMGNPKPSVSWIKGDSPLRENSRIALVESSLRHNV 180  
 Db 121 PKTRPPINVKIIIEGLKAVLPCCTMGNPKPSVSWIKGDSPLRENSRIALVESSLRHNV 180  
 QY 181 OKEDAGGYRCYAKNSLGTAVSKVYKLEFEVFAIRILRAPESHNVTFGSFVTLHCTATGIPV 240  
 Db 181 OKEDAGGYRCYAKNSLGTAVSKVYKLEFEVFAIRILRAPESHNVTFGSFVTLHCTATGIPV 240  
 QY 241 PTTWIENGNAVSSGSIOESYKDVYDSRLQFLTTRKGLYCIAATNKHGEKFSRKAAT 300  
 Db 241 PTTWIENGNAVSSGSIOESYKDVYDSRLQFLTTRKGLYCIAATNKHGEKFSRKAAT 300  
 QY 301 ISIAEMSKPQDNKGYCAQYRGEVCNAYL-----AKDALVEL-NTSYADPEAOELLVHT 354  
 Db 301 ISIAEMSKQKDSQGYCAQYRGEVCNAYL-----AKDALVEL-NTSYADPEAOELLVHT 357  
 QY 355 AMNELKAVSPVCPRAEALLCNHIFQECSPGVPTPIICREYCLAVKELFCAKEMLYME 414  
 Db 355 AMNELKAVSPVCPRAEALLCNHIFQECSPGVPTPIICREYCLAVKELFCAKEMLYME 417  
 QY 415 EKHRLGLRSEMHLLSVKCKSLPSMHDPTACARLPHLDYKNKELKTFPPMTSSKPSVD 474  
 Db 415 EKHRLGLRSEMHLLSVKCKSLPSMHDPTACARLPHLDYKNKELKTFPPMTSSKPSVD 477  
 QY 475 IPNLPSSSSSSFSPYPTSMVTIISIMSSFAIVLLITTTLYCCRRRQKMKKRESAY 534  
 Db 475 IPNLPSSSSSSFSPYPTSMVTIISIMSSFAIVLLITTTLYCCRRRQKMKKRESAY 536  
 QY 535 TLTTLPSSELLDRHPNMYQRMPLLNPKLLSLEYPNNTIEYVADIGEAGFGRFOARA 594  
 Db 535 TLTTLPSSELLDRHPNMYQRMPLLNPKLLSLEYPNNTIEYVADIGEAGFGRFOARA 596  
 QY 595 PGLLPYEPFTWAVAKMLEEASADQADFOREAALMAFNDPNYIKLLGVCAYGKPMCLL 654  
 Db 595 PGLLPYEPFTWAVAKMLEEASADQADFOREAALMAFNDPNYIKLLGVCAYGKPMCLL 656  
 QY 655 FEYMAVGDNLNEFLRSMSPHTVCSLSHSDLSMPAOVSSGPPPLSCAEQLCIARQVAAAMA 714  
 Db 655 FEYMAVGDNLNEFLRSMSPHTVCSLSHSDLSMPAOVSSGPPPLSCAEQLCIARQVAAAMA 716

715 YLSEKFEVHRLDTRNCLVGENMVKIADFGLSRNIYSADYKANEENDAIPIRMMPRESI 774  
 717 YLSEKFEVHRLDTRNCLVGENMVKIADFGLSRNIYSADYKANEENDAIPIRMMPRESI 776  
 775 FYNRYTSDVAVGVVLMFEISYGLQPYGMAHEEVIYVBDGNILSCPEPCPELYNL 834  
 777 FYNRYTSDVAVGVVLMFEISYGLQPYGMAHEEVIYVBDGNILSCPEPCPELYNL 836  
 835 MRLCWSKLPADRPSTSHRILERMCEAREGT 866  
 837 MRLCWSKLPADRPSTSHRILERMCEAREGT 868  
 RESULT 3  
 tor-related receptor rtr - Pacific electric ray  
 N:Contains: protein-tyrosine kinase (EC 2.7.1.12)  
 C:Species: Torpedo californica (Pacific electric ray)  
 D:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 19-May-2000  
 C:Accession: A47299  
 R:Jennings, C.G.; Dyer, S.M.; Burden, S.J.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 2895-2899, 1993  
 A:Title: Muscle-specific trk-related receptor with a kringie domain defines a distinct  
 A:Reference number: A47299; MUID:93219391  
 A:Accession: A47299  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-946 <JEN>  
 A:Cross-references: GB:111311; NID:9290857; PIDN:AAA9285.1; PID:9290858  
 A:Experimental source: electric organ  
 A:Note: sequence extracted from NCBI backbone (NCBI:128724, NCBI:128726)  
 C:Superfamily: Torpedo rtr-related receptor; immunoglobulin homology; kringie homology;  
 C:Keywords: ATP; glycoprotein; kringie; phosphotransferase; transmembrane protein; tyrosine  
 E:4-103/Domain: immunoglobulin homology <IM1>  
 E:137-195/Domain: immunoglobulin homology <IM2>  
 E:229-287/Domain: immunoglobulin homology <IM3>  
 F:464-542/Domain: kringie homology <KR3>  
 F:572-588/Domain: transmembrane #status predicted <TM>  
 F:650-940/Domain: protein kinase homology <KIN>  
 F:658-666/Region: protein kinase ATP-binding motif  
 F:225,340,477,544/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.4%; Score 2897; DB 1; Length 946;  
 Best Local Similarity 59.9%; Pred. No. 8,3e-138;  
 Matches 571; Conservative 113; Mismatches 169; Indels 100; Gaps 11;

5 VNIPVHILTLVAFSGTEK-LPKAFVITPTLETVDALVEEVAIFMCAVESYQPEISWT 62  
 6 VDIPLMIF-LVTTGSGASGILPKAPQITSPLETDALVEEASFCVADSYPAAEITWT 64  
 63 RKILIKLEDTKSTIRENGOLITLSEVSDGICCTANNGVGAESGALQVMMKPK 122  
 65 RNNIPRPFDTKSTIRENGOLITLSEVSDGICCTANNGVGAESGALQVMMKPK 124  
 123 ITRPPINVKIEELKAVLPCTTMGNPKPSWIKGDSPLK-EMSRVLAEGSSLRIRHNO 181  
 125 ITRPPIDVRLKLSKVLPCTTMGNPKPSWIKGDSPLK-EMSRVLAEGSSLRIRHNO 184  
 182 KEDAGQRCVAKNSLGTAVSKVVKLEFEVFAIRLAPESHNTVTFGSFVTLHATGPIPV 241  
 185 LEDAGYRCVAKNSLGTAVSKVVKLEFEVFAIRLAPESHNTVTFGSFVTLHATGPIPV 244  
 242 TTIWINGANAVSSGSDIOESKDVIRDLFTTKRELITCITNKHGEFSTAKAAT 301  
 245 TTIWINGANAVSSGSDIOESKDVIRDLFTTKRELITCITNKHGEFSTAKAAT 304  
 302 SIAMWSPKDNKGVCQYGVYCNVAVLAKDALVFLNTSYADEEAOELVHTAMNELKV 361  
 305 DIKEM-RLYKGDIGCTGYGECQGLNGOLVFNFSFADAEQDQEMARSTWELDG 363  
 362 VSPVCPRAEALLCNHIFQECSP-GVVPTRPIPICREYCLAIVKELFCAKEMLVMEKTHRG 420

364 VILCKPAESELCHFIPODCNPGLGTPKLVCREHCLAVKELCYKEMITMEDNSRIG 423  
 421 LYRSEMHLLSVKCKSLKSMHMDPTACARPLHD-----YKNENL----- 460  
 424 VYSAG--LSLPDCORLPSIHDDPEACTVFSFLDMKGLVTRMCTYNNNGRFYQGSVNTA 480  
 461 -----KTPPMTS----- 469  
 481 SGISGORMEQAHPHRRRLPELPELANDNCRNPGESERPMCTYMDROIRMECNVP 540  
 470 -----KPSVDIPNLSSSSSSSVPTYSMTVYIISMSFAIFVLLITTYVC 518  
 541 QCINVSISEMKPTEANTPSTSA-----TYSMTVYIISMSFAIFVLLITTYVC 593  
 519 RRRKMKKK--RESAVALTTLPSPELLDRLHPNPMORMLLPKLSLEYPRNIE 576  
 594 HHQGLQTKRSYRTETPLATLPSELLDRLHPNPMORMLLPKLSLEYPRNIE 653  
 577 YVRDIGEGAFGVFQARAPGLPEPFTVAVKMKLEASADQADFOREALMAEFNDP 636  
 654 YVRDIGEGAFGVFQARAPGLPEPFTVAVKMKLEASADQADFOREALMAEFNDP 713  
 637 NIVKLLGVCAVCKPMCLFEYVAYGDLNEFLSMSPTVCSLSHSDLSNRQVSSFCPP 696  
 714 NIVKLLGVCAVCKPMCLFEYVAYGDLNEFLSMSPTVCSLSHSDLSNRQVSSFCPP 773  
 697 LSCADQLCARQVAGMAYLSERKFPVHRLDTRNCLVGENMVKIADFGLSRNIYSADY 756  
 774 LSCADQLCARQVAGMAYLSERKFPVHRLDTRNCLVGENMVKIADFGLSRNIYSADY 833  
 757 KANENDAIPIRMMPRESIFNRYTSDVAVGVVLMFEISYGLQPYGMAHEEVIYVR 816  
 834 KANENDAIPIRMMPRESIFNRYTSDVAVGVVLMFEISYGLQPYGMAHEEVIYVR 893  
 817 DGNILSCPEPCPELYNLMLRCLWSKLPADRPSTSHRILERMCEAREGTVS 869  
 894 DGNILSCPEPCPELYNLMLRCLWSKLPADRPSTSHRILERMCEAREGTVS 946  
 RESULT 4  
 A45082  
 neurotrophic receptor ror1 precursor - human  
 N:Contains: protein-tyrosine kinase (EC 2.7.1.12)  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 19-May-2000  
 C:Accession: A45082  
 R:Maslakovskii, P.; Carroll, R.D.  
 J. Biol. Chem. 267, 26181-26190, 1992  
 A:Title: A novel family of cell surface receptors with tyrosine kinase-like domain.  
 A:Reference number: A45082; MUID:93100347  
 A:Accession: A45082  
 A:Molecule type: mRNA  
 A:Residues: 1-937 <MAS>  
 A:Cross-references: GB:M97675; NID:9337464; PIDN:AAA60275.1; PID:9337465  
 A:Note: sequence extracted from NCBI backbone (NCBI:120916)  
 C:Genetics:  
 A:Gene: NTRK1  
 A:Cross-references: GDB:136453  
 A:Map position: 6p21-6p21  
 C:Superfamily: neurotrophic receptor ror; immunoglobulin homology; kringie homology;  
 C:Keywords: ATP; glycoprotein; kringie; phosphotransferase; transmembrane protein; tyrosine  
 F:1-23/Domain: signal sequence #status predicted <SIG>  
 F:24-937/Domain: neurotrophic receptor ror1 #status predicted <TM>  
 F:72-133/Domain: immunoglobulin homology <IM1>  
 F:313-391/Domain: kringie homology <KR2>  
 F:404-425/Domain: transmembrane #status predicted <TM1>  
 F:471-753/Domain: protein kinase homology <KIN>  
 F:47,66,184,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.7%; Score 899; DB 2; Length 937;  
 Best Local Similarity 31.5%; Pred. No. 8,4e-38;

Matches 229; Conservative 102; Mismatches 254; Indels 142; Gaps 20;

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QY 221 HNWV--FSGFVTLHCTATGIPPTTIWENGNAVSSGSIQESKVDKRVIDSRLQ--LFIT 275
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 65 NNITSLQGTALHCKVGNPNPTIRMKNDAPVQVEPRRLSFRSTIYSRIRINLDTT 124
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 276 KPGLYTCATNKGKKESTAKAATISTIAEMSKP---QKDNKGCAQYREVCNAVLAK 331
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 125 DTGYEQCATNGKEVYSTGVLFVFCGPPPTASPGYSEYEDGFCQYRGIAC--ARRIG 183
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 332 DALVFLNLSYADPE--EAEELVHTMTMNLKVSPYCRRAEMLCNHIFQEC--SGVVP 389
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 NRTVMESLMHOGELIENITAFMTIGTSSHSDKCSGFALPSICHYAFPCDETSSVPK 243
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 390 PIPICREYCLAVKELFCAKEMLVMEKTHRGLYRSE---MHLLSVKCSKILPSMHMDPTA 446
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 PRDLRCRDECELLENVLCQETYL-----FARSNPMILMRKLPNCEDLPQEPSPRA 294
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 447 -CAR--LPHLDYKNENLKT-----PPMTSSKPSV----- 473
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 295 NCIRIGTMAPDPIKNHKCNSTGVYRGVSVTKSGRCQCPWNSQYEHHTFTALRPE 354
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 474 -----DIPNLPSSSSSPSFVSPTSMVTIISIM 501
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 355 LINGHSYCRNPGNCKEAPWCFTLDENFKSDLCDIDPACDSKSKEN-----KMEIYLIV 409
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 502 SSFAIEVLLTITLYCCRRRQMKKKRESAAVLTTLPSLELLDRHPNMYQMP--- 558
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 410 PSVAIPALAILFFFCVCR---NNOKSSAPV-----QROPKHV 446
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 559 -----LLLN---PKLILEYPRNNIEYVVDIGEGAGRGVQAR--APGLPEPFTMV 606
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 447 RGQVEMSLMAYPKSKAKELPLSAVMEELDECAKGLYKGLYLPGM---DHAOLV 503
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 607 AVKMLKEASADMOADPQREALAAEFDPNPITVLLGCAVCAKPMCLIEFYMAVDNEF 666
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 504 AIKTLKDYNNQOMMEFQGEASLMAELHHPNITVCLLAVNOEOPVCMLEFIINGDLHEF 563
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 667 LRMSPTVCSLSHSDLSMRAQVSSPGPPPLSCAEQCLIAOVAAGNAVLSERKRVHDL 726
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 564 LIMSPP-----HSDVGCSSDEDEGTAKSSLDHGDPLHAIQIAAGMEYLSHFVHDL 616
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 727 ATRNCIVGENNVVITADFGSLRNITYSADYKANKENDAIPIRMPESTFYRTTESDVM 786
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 617 AARHILIGEOUHVAKISDLGSLREIYSADYKRVQSKSLPIKMPPEALIMGKFSDDDIW 676
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 787 AYGVVLMEISYGLQPYGMAHEEVIYYVRDGNILSCPENCPVELYMLMLRCLPADR 846
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 677 SFGVVLMEISFGLQPYGFSNGEVIEMVRKROLLPCESECPRMYSILMECHNEIFSR 736
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 847 PSFTSIH 853
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 737 PRFKDIH 743
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

# RESULT 5

B45082  
 A:neurotrophic receptor for2 precursor - human  
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)  
 C:Species: Homo sapiens (man)  
 C:date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 19-May-2000  
 C:Accession: B45082  
 R:Maslakovskiy, P.; Carroll, R.D.  
 J. Biol. Chem. 267, 26181-26190, 1992  
 A:title: A novel family of cell surface receptors with tyrosine kinase-like domain.  
 A:reference number: A45082, M01D:93100347  
 A:Accession: B45082  
 A:molecule type: mRNA  
 A:residues: 1-943 <MAS>  
 A:cross-references: GB:M97639, NID:q337466, PIDN:AAA60276.1, PID:q337467  
 A:note: sequence extracted from NCBI backbone (NCBIP:120918)  
 C:genetics:  
 A:gene: GDB:NTFRK2

A:Cross-references: GDB:136454

A:Map position: 6p21-6p21  
 C:Superfamily: neurotrophic receptor for immunoglobulin homology; kringle homology;  
 C:Keywords: ATP; glycoprotein; kringle; phosphotransferase; transmembrane protein; ty  
 F:1-27/Domain: signal sequence #status predicted <Sig>  
 F:28-937/Product: neurotrophic receptor for2 #status predicted <Mat>  
 F:76-137/Domain: immunoglobulin homology <IM>  
 F:316-394/Domain: kringle homology <KR>  
 F:412-428/Domain: transmembrane #status predicted <TM>  
 F:471-753/Domain: protein kinase homology <Kin>  
 F:479-487/Region: protein kinase ATP-binding motif  
 F:70,188,318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.2% Score 876; DB 2; Length 943;  
 Best Local Similarity 28.6% Pred. No. 1.2e-36;

Matches 236; Conservative 119; Mismatches 249; Indels 222; Gaps 26;

```

QY 126 PPIVWIKIEGLKAVLPCTMGNPPRSVWIKGSDPLRENSRIAVL---ESGS-LRIHNVQ 181
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 67 PNNITIVOGTALHCKVAGNPNPPVWMLKNDAPVQVEPRRIIRKTEYGRRLRIDLD 126
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 182 KEDAGQRCVAKNLSGLTAYSKVYVLEFEVFAKILRAESHNVGTGFTLCTATGTPVP 241
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 127 TDTGYQCVATNGMKT----- 149
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 242 TITWENGNAVSSGSIQESKVDKRVIDSRLQFLTRKPGLYCIATNKGKFSFAKATI 301
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 150 -----LTV----- 158
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 302 SLAEMSKPQDKNKGCAQYRGECVNAVLANDALVELNTSADPEAO--ELLVHTMANE 358
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 159 SPNNHFDYDEHDFCCPYRGIAICARFIGN---RTIYVDSLOMGEIENRTITAFMT 212
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 359 LKV---VSPICRAAEALLCNHIFQEC--SPGVVPTPIPIREYCLAVKELFCAKEMLVME 414
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 213 IGSTHLSDDCSQFALPSFGHVFPLDANSRAKPRELCREVEVLESDLCQETIYA- 271
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 415 EKHRLGYSR---MHLLSVKCSKILPSMHMDPTA--CARLP-----HLDYN--- 456
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 272 -----RNPILMLRLQPLKCEALP--MPESPANACMIGIPIAERLGRYHQCYNSSGM 322
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 457 -----KENLKTTP-----PMTSSKPSVDIPNT----- 478
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 323 DYRGTASTYKSGHCQCPWALQHPHSHLSSTDPELGGHAYCRNPGQMECPWCTQNK 382
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 479 -----SSSSSSPSFVSPTSMVTIISIMSFAT--FVLLITITLYC--CRRKQMKNK 527
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 383 NVRMELCDVPSCSPROSS-----KMGILTYLVSAIPVIAICFLVLCMKR-----NK 431
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 528 KRSSAAV---TLTLPSELLEDRHPNMYQMPPLLNKLSTL--EYPRNNIEYVDIG 582
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 432 QKASASTPQGRQLMASPSQDM-----EMPLINQKQAKLKEISLSAVERFELG 480
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 583 EGAFGRVFOARAPGLLPYEPFTWAVYAKMLKEASADMOADPQREALAAEFDPNPITV 642
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 EDRFGKYKHLRGPAVGEOTOVAIKTLKDAEGPLREFEERHEAMLRALQHPNVCLL 540
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 643 GVCVAVGKPMCLLEFYVAYGDLNEFLRMSPHPTCSLSHSDLSMRAQVSSPGPPPLSCAD 702
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 GVTYTKDPLMTISYCSHGDLHEFLVMSPHSVGSTDIDRYKSALEPP-----DF 592
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 703 LCIAROVAAGMAYLSERKFNHRDLATRNCLVGENNVYKIDAFGLSNITYSADYKANKEND 762
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 593 VHLVAQIAAGMETLSHHVYHNRKLAIRNVLYTKLVAKVTSDLGLFEVYAAADYTKLLGNS 652
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 763 AIDIRMPPESTIFYNRTTESDYMAVYVLMELFSYGLQPYGMAHEEVIYYVRDGNILS 822
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 653 ILPIRMNAPPAIIMYGKFSIDSDIMSYGVYVLMELFSYGLQPYGYSNODVEMIRNQVLP 712
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 823 CPENCVEVLYNMLRCLWASKLPADRPSTSIHRLLEMKERASTVTS 868
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 713 CPDDCEAWVYALMIDCMENFPSPRRPRFKDIHSRL-----RAMGNLS 753
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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OY 409 EKLWVEEKTRHRLTYSEMHLVSPKCSKLPKSHMHMPRTACARPLHIDYKKNENKATPPRPTS 466
Db 399 DMTT-----PDIIGDT-----NKS----- 414
OY 469 SKPSVDIPNLPSSSSSFSPSPYGMTVIISMSFAIFVLTITTLTYCCRRKQMKNK 528
Db 415 EIPSPDVA--OSNREHLSV--YAVVIASVVG---FCLLVMLLLKLARHSFGK 465
OY 529 RESAAVTITLPSSELLDRLHNPYQ-----RNPILLNKL 565
Db 466 PASV-----ISNDDDSASPLHHSNCSNTPSSSEGGDAVIGMTKIPYENFOY 515
OY 566 ISL-----EYPRNNIEYVRDIGEGAFGCFPOARAGLLPPEPFPMVAWKME 613
Db 516 FGIINSQKLPDFFVGHIRKRNHIVLKRLEGEGAFGVFLAECCYNLCPEBDKILVAVKTLK- 574
OY 614 EKSAMQADFOREALMAEFDPNPIVTKLGCANGKRPMLLFETWYADLNEFLKMSPH 673
Db 575 DASDARRKDFHEAEGLTNLOHEHIVKEVCVEDDPLIMVEYWKHODLKLFLAHPD 634
OY 674 TVCSLSHSDLSMRACVSSPPPP--LSCAEOLCIARQVAAAGVAYSEKFPNRDLATRNC 731
Db 635 AV-----LMAEGNPTELTQSOMLHITQIQAAGNVILASGHPHNRDLATRNC 681
OY 732 LVGENMYVKIADFGLSRNITYSADYKANKENDAPIRPMRPESIFNYRTTESDWAYGV 791
Db 682 LVGENMLVKIGFGMSRBYSTDYRVGFGHMLPIRPMRPESIMRKRTTESDWAYSLVV 741
OY 792 LWEIFSYGLOPYGAAHEEVIYYVADGNILSCPEKCPLELNLWRLCKSKLPAPRPSPTS 851
Db 742 LWEIFTYGRKQRYQYCSNNEVIECTIGRNVLRQPRCPQEVYELMLGCHQREPHRKNIKS 801
OY 852 IHRILERMCE 861
Db 802 IHTLQNLAK 811

RESULT 7
A:Residues 56853
brain-derived neurotrophic factor receptor precursor - human
N:Alternate names: receptor tyrosine kinase
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Homo sapiens (man)
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 11-Jun-1999
C:Accession: A56853
R:Nakagawa, A.; Liu, X.G.; Ikegaki, N.; White, P.S.; Yamashiro, D.J.; Nycum, L.M.;
Genomics 25, 538-546, 1995
A:Title: Cloning and chromosomal localization of the human TRK-B tyrosine kinase rece
A:Reference number: A56853; MUID:95309922
A:Accession: A56853
A:Molecule type: mRNA
A:Residues: 1-822 <NAK>
A:Cross-references: GB:U2140; NID:g525313; PIDN:AAC51371.1; PID:g530791
R:Shelton, D.L.; Sutherland, J.; Gripp, J.; Camerato, T.; Armanini, M.P.; Phillips, H
J. Neurosci. 15, 477-491, 1995
A:Title: Human trks: molecular cloning, tissue distribution, and expression of extrac
A:Reference number: I56557; MUID:95123473
A:Accession: I56557
A:Status: preliminary: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-822 <SHF>
A:Cross-references: GB:S76473; NID:g913717; PIDN:AAB3109.1; PID:g913718
C:Genetics:
A:Gene: GDB:MTRK2; trkB
A:Cross-references: GDB:127898; OMIM:600456
A:Map position: 9q22.1-9q22.1
C:Function:
A:Description: regulation of nervous system development; receptor for brain-derived n
C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glyc
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth fact
inase
-1-31/Domain: signal sequence #status predicted <Sig>

```

F:32-822/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>  
 F:32-435/Domain: extracellular #status predicted <EXT>  
 F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F:436-452/Domain: transmembrane #status predicted <TM>  
 F:453-822/Domain: cytosolic #status predicted <CYT>  
 F:536-814/Domain: protein kinase homology <KIN>  
 F:544-552/Region: protein kinase ATP-binding motif  
 F:67,99,121,178,205,241,254,280,335,338,350,412/Binding site: carbohydrate (Asn) (covalent)  
 F:572/Active site: Lys #status predicted  
 F:706/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted  
 F:817/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 18.8% Score 861 DB 1 Length 822  
 Best Local Similarity 29.5% Pred. No. 5.9e-36;  
 Matches 253; Conservative 115; Mismatches 269; Indels 222; Gaps 30;

59 ISWTRKILKLPDTRYSIRENGQL-----TILSYEDSD--GIYCCT 100  
 120 INFTRNK-LTSLSKHRRHDLSELILVGNPFTSCDIMATKTIOEAKSSPDODICLN 178  
 101 ANNG-----VGGAVESGALGVKMKPKITRPINVKIIEGLKAVLPCTMGNPKPSVSWIK 156  
 179 ESSKNIPLANQIPNCGI-----PSANLAPNLTVREGKRSITLSCVAGDPVPMWMDV 232  
 157 GD---SEPREKRIAVLESGLRHNQOKDAG-QYRKVANNSIGTASVY-VKLEFVYF 211  
 233 GNLSVKHNNETSH---TQGLRITNIISSDSGKQISCAVNLGVEDDSVNLVHFAPT 288  
 212 ARIAPRESH---VTFGSFYLHCTAGIPVPTITLNGNNAVSSGSIQDSVDRVADS 268  
 289 ITFLESPTSDHMCIPF-----TYKGNPKPALQWYNG-ALINEKYLCTIHLHTVNH 339  
 269 R-----IQLFTTKP-----GLTYCIATNKG--EKSTAKAATISAEWSKPO-----K 311  
 340 TEYHGCIQL--DNPTLHMNGDYTLIAKNEYKQISAHMCPMGIDDAGPNVPIY 397  
 312 DNKGYCAQYRGVGNNAVIAKALVFLMNSYADPEAOGLVHTMNLKLVSPICRPAE 371  
 398 EDYGTANDIGDTTNR-----SNEIPSTDVTKGRELISYAVVAVIASVG----- 444  
 372 ALLCNHIFQESGCVVPVPIPIRECYCLAVELCAKEMLEMERKTHGLRSEMHLSV 431  
 445 -----FCI-----LVM-----LFLKL 456  
 432 PKCSKL---PS--MHMDPACARLPHLDYKNEMLKTFPMTSSKPSVDITNLPSSSSS 485  
 457 ARHSKFGKGPASVYISNDSDSAPLHHSNGS-----NTPSSSGG 497  
 486 FSVSPYTSMTYIISMSFAIFVLLTITLVCCRRRKQMKKRESAVALTLTPSELL 545  
 498 -----PDVATIGMTKP----- 509  
 546 DRLHPNRYQMP-LLNPKLLSLEPRNIEYVADIGEGAFGRVFOARAGLLPYEPT 604  
 510 --VIENPQYFGITNSQLPDTFFVQHIKRHNIIVLKRELEGCAFGLAEACYNLCPEODKI 567  
 605 MVAAYKMLEKESADMOADFOREALMAEFDPNIVYKLLGVCAVGKPKMLLEFYAAGDNL 664  
 568 LVAATKTK-DASDNARKKPFHREAEELLTNLQHEHIVKFGVCEVGGDPLLMVEEYMKHGLN 626  
 665 EFLSMSPHTYCSLSHSDLSKRAOVSSPPRP--LSCAEQICIAROVAAGAAVYSERFV 722  
 627 KEFLAHAGDAY-----LMAEGNPTELTSQMHIAQIAGAVVYIASQHFV 673  
 723 HRDLATRNCLVGENNVYKIADFGLSRNYSADYKRAKENDAIPIRMPPEISIFNRYTTE 782  
 674 HRDLATRNCLVGENNLVYKIGDFGMSRDVYSPDYRVGSHTMLPIRMPPEISIMYKFTTE 733  
 783 SDVAVYGVLMLEISYGLPIYGAHAEVYIYVVDGNILSCPENCPVELLYNMLRCLMSKL 842

Db 734 SDVMSLGVLMLEIPTYKOPWYQLSNNEVICITQGRVLOPRPCPOVEYELMGWORE 793  
 QY 843 PADRPSTSHRIELRMCE 861  
 Db 794 PHMKRNKIGHTLQNLAK 812

RESULT 8  
 S44098  
 brain-derived neurotrophic factor receptor precursor - chicken  
 N:Alternate names: receptor tyrosine kinase trkB  
 N:Contains: protein-tyrosine kinase (EC 2.7.1.112)  
 C:Species: Gallus gallus (chicken)  
 C:Date: 13-Jan-1995 #sequence, revision 13-Jan-1995 #text, change 11-Jun-1999  
 C:Accession: S59939; S42175; S44098  
 R:Vinh, N.O.; Erdmann, K.S.; Heumann, R.  
 Gene 149, 383-384, 1994  
 A:Title: Cloning and sequence analysis of a cDNA encoding a novel truncated form of t  
 A:Reference number: S59938; MUID:95047511  
 A:Accession: S59939  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-818 <VI2>  
 A:Cross-references: EMBL:X77251; MID:9563881; PIDN:CA54468.1; PID:9472934  
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994  
 R:Dechant, G.; Biffo, S.; Okazawa, H.; Kolbeck, R.; Pottgiesser, J.; Barde, Y.A.  
 Development 119, 545-558, 1993  
 A:Title: Expression and binding characteristics of the BDNF receptor chick trkB.  
 A:Reference number: S42175; MUID:94116452  
 A:Accession: S42175  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-818 <DEC>  
 A:Cross-references: EMBL:X74109; MID:9407798; PIDN:CA542210.1; PID:9407799  
 A:Gene: trkB  
 A:Function: regulation of nervous system development; receptor for brain-derived n  
 C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glyc  
 C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth fact  
 inase

F:31/Domain: signal sequence #status predicted <SIG>  
 F:32-818/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>  
 F:32-433/Domain: extracellular #status predicted <EXT>  
 F:66-90/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>  
 F:91-114/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>  
 F:115-137/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>  
 F:138-149/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical  
 F:433-449/Domain: transmembrane #status predicted <TM>  
 F:450-818/Domain: cytosolic #status predicted <CYT>  
 F:532-810/Domain: protein kinase homology <KIN>  
 F:540-548/Region: protein kinase ATP-binding motif  
 F:66,94,120,199,204,253,287,324,337,349,408/Binding site: carbohydrate (Asn) (covalent)  
 F:568/Active site: Lys #status predicted  
 F:702/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi  
 F:813/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 18.8% Score 858 DB 1 Length 818;  
 Best Local Similarity 29.4% Pred. No. 8.2e-36;  
 Matches 262; Conservative 118; Mismatches 281; Indels 230; Gaps 35;

6 NIPLVHT-LTLVANSGETKLPKAVYITTPLETVDALVEVATFKCAVSYQPEISWTRN 64  
 Db 113 NINIOYIMLSRNKLSLSKKPFRIHGLSLDILYD-----NPFKSC-----ELMWIK- 159  
 QY 65 KILKLPDTRYSIRENGQLTILSYEDSDGIGCTANNNGVAGAVESGALGVKMK----- 120  
 Db 160 ---KFEETKK-----YTEAOD--IYCDVNN-----KRALMDMKVPCNDL 195  
 QY 121 PKTRPPINVKIIEGLKAVLPCTTMGNPKPSVSWI-----KGSPLRENSRIAVLES 174

```

Db 196 PSANISNITIVYEGSKITLYCDTGGPPPNVSWVLTNLVNHSDETSKN-----PAS 248
Oy 175 LRIHNVOXEDAGQY-RCVAKNSLGTAYSKYVKLEFEVFARILRAPESHVTFGSEVY---- 230
Db 249 LTIKNVSSDGLMISCAVENIVGEVQISA-----ELTVF-----AP---NITFLESTPPH 298
Oy 231 ---LHCTATGIVPPTIYIENGNAVSSGISQGSVDRIISR-----IQLEFTTKP----- 277
Db 299 HWCIFPTVGNPKPTLQWVEEG-ALLNESEYICTKIHVINOSEYHQCQLD--DNPTHLNN 355
Oy 278 GLYTCIATNKHGEKSTKMAATISIAEMSKQKONKGCACAYR---GEVCNANVLAKDL 334
Db 356 GAVTLAKKEGE-----DEKRVDAHFMSVPGSGSPITDPDY 394
Oy 335 VFLNTSVADPEEAQELLVHTANNEKLVSP-VCPRAEALLCNHIFFQECSPGVPTPIPI 393
Db 395 EYETI-----PND-----LQGTNNNSNOITSPDYSNKNENESTIYV-----VCGIALV 439
Oy 394 CREYCLAYKELFCAKEMVMEKTRGLYRSEMHLISVPKSKLPS--MHMDPTACARLP 451
Db 440 CTGLVIML-----IILKFGRI-----SKFGM-----KGPSVISNDODSAPLH 478
Oy 452 HLDYKKNELKTPPMTSSKPSVDIPNLPSSSSSSFVSPTYSMTVYIISMSSFAIFVLLT 511
Db 479 HISNKS-----NTPSSSEGG----- 493
Oy 512 ITTLVCCRRRQWKKKRESAAVLTTLTLPSELLDLRHPNMYQWRP-LLLNPKLISLEY 570
Db 494 -----PDAVITIGMTKIP-----VIENPOLYFGITNSQLKPDIFVQHI 529
Oy 571 PRNIEYVADIGEGAFGVFOFARGLLPYEPFTVAVKMKLEKESADMOQDFOREALM 630
Db 530 KRNHIVLKRLEGEAGFVGFYLAECYNLCPEODKILVAVKTKL-DASDNARKFHEAEELL 588
Oy 631 AEFDPNIVKLGVCAGVAKPMLFEYMAVAGDLNEFLRSMSPHTYCSLSHSDLSMRAQVS 690
Db 589 TNLQHEHIVKFGVCEVDPLIMVEFYMKHODLNKFLRAHGRDAY-----LMAE 637
Oy 651 SPGRPLSCAEQDLCTAROVAAGMAYLSERKRVHDLATRNCLVGENNVYKADFGLSRNI 750
Db 638 GNRPAELTQOSQMLHTAQOIAAGMVYLAHQHFNHDLATRNCLVGENNLVYKIDFGMSRDY 697
Oy 751 YSADYKKNANDALPIRMMPRESIFYNRYTTESDYVAVGVVMEFSGLOQYXMAHBE 810
Db 698 YSTDYIRKGGHTMLPIRMMPRESIYRKFTTESDVSGLVAVLWELFTYQKQWYDLSNE 757
Oy 811 VIVYVRDGNILSCPENCPVELYINMLRCLMSKLPADRPSTSIHRIERKCE 861
Db 758 VIECTQGRVLOPRPCPKVEYVDLMLGCMQREPHMRMLNIKEHSLQNLAK 808

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RESULT 9
A39667
brain-derived neurotrophic factor receptor precursor - rat
N:Alternate names: receptor tyrosine kinase trkB,FL
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 27-Nov-1991 #sequence,Leviston 27-Nov-1991 #text,change 11-Jun-1999
C:Accession: A39667
R:Middlemas, D.S.; Landberg, R.A.; Hunter, T.
Mol. Cell. Biol. 11, 143-153, 1991
A:Title: trkB, a neural receptor protein-tyrosine kinase: evidence for a full-length and
A:Reference number: A39667; MUID:91094826
A:Accession: A39667
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-821 <MID>
A:Cross-references: GB:M55291; NID:g207473; PIDW:AAA42279.1; PID:g207474
C:Function:
A:Description: regulation of nervous system development; receptor for brain-derived neu
C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycop
C:Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; growth factor
inase

```

```

F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-821/Product: brain-derived neurotrophic factor receptor #status predicted <MAT>
F:32-434/Domain: extracellular #status predicted <EXT>
F:67-91/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:92-115/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:116-138/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:139-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
F:435-451/Domain: transmembrane #status predicted <TMN>
F:452-821/Domain: cytosolic #status predicted <CTT>
F:535-813/Domain: protein kinase homology <KIN>
F:543-551/Region: protein kinase ATP-binding motif
F:67,95,121,178,205,241,254,280,325,338,350,411/Binding site: carbohydrate (Asn) (cov
F:705/Active site: Lys #status predicted
F:705/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi
F:816/Binding site: phosphate (Tyr) (covalent) #status predicted

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```

Query Match 18.7%; Score 854.5; DB 1; Length 821;
Best Local Similarity 28.3%; Pred. No. 1.2e-35;
Matches 249; Conservative 113; Mismatches 254; Indels 263; Gaps 30;

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Oy 59 ISWTRNKILIKLPDRYISRE-----NGQ-----LLTLYVEDSD--G 95
Db 120 INFTRKTL-----TSLSRHFRHLDLSDLLTGNEFTSCDIMMLKTLQETKSSPDTD 173
Oy 96 IYCCTANNQ-----VGAVERSGALQVKKMKRITRPPIYKIIIEGLKAVLPCTTGNPKPS 151
Db 174 LYCLNBSKNTPLANLQIPNGL-----PSARILAPNLTVREGSKSVTISCVGDDPLPT 227
Oy 152 VSWIGD---SPLRENSRIAVLESGSLRIHNVOXEDAG-QYRCVAKNSLGTAYSKY-VKL 206
Db 228 IYMDVGNLVSKIMNETSH---TQGLSRITNTSSDSQKQICVAENLVGEQDSDSNVLT 283
Oy 207 EEFVFARILRAPESHN---VTFGSEVTLHCTGTGIPVPTIYIENGNAVSSGISDESVD 263
Db 284 HNPATITPLESTSDHNCIPF-----TYRGNPKPALQWFGNG-ALLNESKIYCTKI 334
Oy 264 RVIDSR-----IQLEFTKP---GLYTCIATNKHGE-----KFTAKAA 298
Db 335 HVTNTEHYGCLQ--DNPTHMNGDYTLMAKNEXGKDERQISAHFMGRPGVDYENPAY 392
Oy 299 ATISIAEMSKP-----QDNKGYCAQYRGVCNANVLAKDLVFLNLSYADPEEAQELL 351
Db 393 PEVLIEDWTPPTIDGDTTKNSNE-----IPSTDVAQDQTNREHLS 431
Oy 352 VTANNEKLVSPVCPRAEALLCNHIFFQECSPGVVPTPIPICREVCLAVKELFCAKEL 411
Db 432 YVAVVVIASVVG-----FCLLVML----- 451
Oy 412 VMEKTRHGLYRSEMHLISVPKSKL---PS--MHMDPTACARLPNLDYKNENIKTPRP 465
Db 452 -----LLKLARHSKFGMKGPASVISNDODSAPLHISNKS----- 487
Oy 466 MTSSKPSVDIPNLPSSSSSSFVSPTYSMTVYIISMSSFAIFVLLTTLVCCRRRQW 525
Db 488 -----NTPSSSEGG----- 496
Oy 536 NKKRESAAVLTTLTLPSELLDLRHPNMYQWRP-LLLNPKLISLEYPRNIEYVADIGEG 584
Db 497 ---PDAVITIGMTKIP-----VIENPOLYFGITNSQLKPDIFVQHIKRNHIVLKRLEGB 546
Oy 585 AFGRFQARARGLLPYEPFTVAVKMKLEKESADMOQDFOREALMAEFDNPNIYKLG 644
Db 547 AFGKVFLEACYNLCPEODKILVAVKTKL-DASDNARKFHEAEELLTNLQHEHIYKFGV 605
Oy 645 CAVGKPMCLFEYMAVAGDLNEFLRSMSPHTYCSLSHSDLSMAQVSSGPRP--LSCAEQ 702
Db 606 CVEDPLTLMVEFYMKHODLNKFLRAHGRDAY-----LMAEGRPTETLQOSOM 652
Oy 703 LCIAROVAGMAYLSERKRVHDLATRNCLVGENNVYKADFGLSRNIYSADYKANEED 762
Db 653 LHIHQOIAAGMVYLAHQHFNHDLATRNCLVGENNLVYKIDFGMSKRDYVSTDYIRVGGHT 712

```







F:433-790/Domain: cytosolic #status predicted <CYN>  
 F:502-782/Domain: protein kinase homology <KIN>  
 F:510-518/Region: protein kinase ATP-binding motif  
 F:67,95,121,188,202,253,262,281,318,323,338,358,395/Binding site: carbohydrate (Asn) (cc  
 F:538/Active site: Lys #status predicted  
 F:674/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predicted  
 F:785/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 17.7%: Score 810; DB 1; Length 790;  
 Best Local Similarity 27.3%: Pred. No. 2e-33;

Matches 254; Conservative 116; Mismatches 257; Indels 304; Gaps 29;

```

QY 1 MRELNIPIVHITLV-----AFSGTEKLPKAPVITPPLTETVDALVEEATFMCA 50
DB 84 LNDLRGLRLTLTKVSGSLRFVAPDAFHPTRLSLNLSFNLES----- 129
QY 51 VESYPPQELSWTRNKILKLFDRYSIRENGQLTLTSLVEDSDGIYCTA-----N 102
DB 130 -----LSW-----KTVGSLQLDELVLGSGNPLHSCCALRMILQRMEE 164
QY 103 NGVGAVF-----SCGALQYKMKPKITRPINVKIIEGLKAVLPCTM 145
DB 165 EELGVPEQKLCQHGCGPLAHMPNASCQVPLTKQYR-----MASVDGDDVLRLCYE 218
QY 146 GMPKPSVSIKQDSPLENSRIA-VLESG-----SLRINVOKE-DAGQYRCVAKNSLGT 198
DB 219 GGLGEOAGMI-----LTELQSATYKSSGSLPSLGLTLANVSDLRKMLTGWAEENDYR 273
QY 199 AVSKVVKLEFEVFAIRILRAPESHNTFGSFVTLHC-----TANGIVPTITWIE 247
DB 274 A-----EVSQV-----NSFPASVOLHTAVENHMSIPESVDGQAPRLRWLF 317
QY 248 NGNAVSSGS-----IQESVKDRVIDSRQLFTKPR-----GLTYCIATNKGEKSTAK 296
DB 318 NGSVNIETSFITEEFLEPANETVRHGCRL--NQPTHVNGNITLLANPPGQ----- 369
QY 297 AATISIAEMSKPQKDNKCYCAQYGEVCNANVLADALVFLVTSADPEAOELVHTAM 356
DB 370 ASASIMAFMDNPFEFN-----PDDPIPDITNSTSDPVEKDD----- 406
QY 357 NELKVVSPVCRPAEALLCNHIFQCSPCGVPTPIPICHREYLAAYKELCAKEMLMEMK 416
DB 407 -----ETPFGVSVAAGLAV--FAC----- 423
QY 417 THRGILYRSEMILSVPKCSKLPSPMHMDPTACARLPHLDYKNKENLTFEPMTSSKPSVDIP 476
DB 424 -----LELSTL-LLVLNKCGR-----RNKFGI-----NRPAVLAP 452
QY 477 NLPSSSSSSF-----SVSPYSMTVIISIMSPAFIVLTTITTLTXCCRRKQMKKKRE 530
DB 453 EDGLAMSLHFMTLGGSSLSPTEG----- 475
QY 531 SAAVTLTLTLPSELRLRHPMPYQRMPLLNPKLLSLEYPRNNITEYRDIEGAGFGRVF 590
DB 476 -----KSGGLQGHIEENPOYPSDACVNHK-----RQDLYLAKWELGEGAFGKVF 519
QY 551 QARAGLLPYEPFTVAVAKMLKEASADQADFOREAAALMAEFDPNITVKLGLGCAVAKP 650
DB 520 LAECNNILPEODKMLYAVKALK-EASESARQDFOREALLTLMQOHILYRFGVCTEGRP 578
QY 651 MCLFEYAAUGDNLNFEFLSMSPHYTCSLSHSDLSMRAYVSSGPPPLSCAEOGLIAROVA 710
DB 579 LLMVFEYRRHDDLNFLRSHSP-----DAKLLAGEDVAPQGLIGOLLAASQVA 629
QY 711 AGMAVLSERKFEVHRDLATRNCLVGENMVVKIADFGLSRNITVSADYVKKANENDAPIIRMP 770
DB 630 AGMYVLAGLHNVHDLATRNCLVQGLVYKIGDGMASDIYSTDYRVRGGKMTLPDIRMP 689
QY 771 PESIFYNNTTESDVMAVGVVLMETFSGLQPYGMAHEEVIYVVRDGNILSCPENCPVE 830
DB 690 PESILYRKFTTESDVMSFGVVLMEIFTYGKQPMYQWOLSNTEAIDCITQRELERPRACPE 749

```

QY 831 LYNLMRLCWSKLPADRPSTSIHRIERMC 861  
 DB 750 VVAIMGQWQREPQORHSIKDVHARLQALAQ 780

RESULT 12  
 S35695

neurotrophin-3 receptor precursor - chicken  
 N:Alternate names: receptor tyrosine kinase trkC  
 N:contants: protein-tyrosine kinase (EC 2.7.1.112)  
 C:Species: Gallus gallus (chicken)  
 C:Date: 10-Dec-1993 #sequence\_revision 03-Nov-1995 #text\_change 11-Jun-1999  
 C:Accession: S35695  
 R:Okazawa, H.; Kamel, M.; Kanazawa, I.  
 FEBS Lett. 329, 171-177, 1993

A:Title: Molecular cloning and expression of a novel truncated form of chicken trkC.  
 A:Reference number: S35695; MUID:93359043  
 A:Accession: S35695  
 A:Molecule type: mRNA  
 A:Residues: 1-803 <OK>

A:Cross-references: EMBL:X59669; NID:9416429; PIDN:CAA42202.1; PID:9416430  
 A:Note: the authors translated the codon AAC for residue 105 as Val, C7G for residue  
 C:Function: regulation of nervous system development; receptor for neurotrophin-3  
 C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glyc  
 C:Keywords: alternative splicing; ATP; autophosphorylation; brain; glycoprotein; grow  
 otein kinase

F:1-10/Domain: signal sequence #status predicted <SIG>  
 F:11-803/Product: neurotrophin-3 receptor #status predicted <ANT>  
 F:11-417/Domain: extracellular #status predicted <EXT>  
 F:58-82/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRB1>  
 F:83-106/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRB2>  
 F:107-129/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRB3>  
 F:130-141/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical  
 F:435-434/Domain: transmembrane #status predicted <TM>  
 F:435-803/Domain: cytosolic #status predicted <CYT>  
 F:514-795/Domain: protein kinase homology <KIN>  
 F:522-530/Region: protein kinase ATP-binding motif  
 F:47,51,58,142,182,197,211,238,246,251,273,354,367/Binding site: carbohydrate (Asn) (cc  
 F:550/Active site: Lys #status predicted  
 F:687/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi  
 F:798/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 17.7%: Score 810; DB 1; Length 803;  
 Best Local Similarity 27.4%: Pred. No. 2e-33;

Matches 221; Conservative 101; Mismatches 214; Indels 270; Gaps 21;

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QY 121 PKITRPINVKITIEGLKAVLPCTMGNPKPSYSWIKGD---SPLENSRIAVLESGSLR 176
DB 189 PEISVSHVLLVREGENAVITCNGSGSLPDDVDMTVADLHSINTHTQNLNMTNVAHAINLT 248
QY 177 IHNQKEDAG-QYRCVANKSLCTAASKYVVKLEFEVFAIRLAPF-----SHAVTGSFVT 230
DB 249 LVNVTSEDGELLTCTIAEIVVGMASNAV-L-LTVYVPRRLTLEBPVLLHLEHCIAF---A 303
QY 231 LHCTATGIVPPTITWINGNAV-----SSGSIQESVKDRVIDSRQLFTKPR-- 277
DB 304 VH-----GNPAPRTLHLNHCQVLRREFTIIMERYQGEVSEGC-----LLENKPTN 349
QY 278 ---GLTYCIATNKHGEKSTAKAAATISIAEMSKPQKDNKGYCAQYRGEVCNAVLAKDAL 334
DB 350 YNNGNYVTIVATNQLSANQITKG----- 372
QY 335 VFLNVSADPEAOGLLVHTAMNELKVVSPVCRPAEALLCNHITFQCSPCGVPTPIPIC 394
DB 373 ----- 372
QY 395 REYCLAIVKELCAKEMLMEMKTHRGILYRSEMILSVPKCSKLPSPMHMDPTACARLPHLD 454
DB 373 -----HLEKRP----- 378
QY 455 YNKENLKTFPMTSSKPSVDIPNLPSSSSSSFVSPTYSMTVI-----ISIMSSFA 505

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Db 379 -----PESTDNEVSI-----GDYVSPPTLTVTHKKPEDTFGSIANGLA 420
QY 506 IFVLLITITLYCC-----RRRKQWKNK-----KRESAAVLTITLPSSELLDRLHPNM 553
Db 421 AFACVLLVAFIMINKYGRSKFGMKGPVAVISGEEDSAATHSTDTREFTVD-AGPDIV 479
QY 554 ----YQRPILLNKLKLSLEY-----FRNNIEYVRDICEGAFGVFOARAGCL 598
Db 480 VIGMTRIPVLENPOYFRQGNCHKPDITYVOHIKRDIKRLRELGEAGFAGVFAECYNLS 539
QY 599 PYEPFTVAVKMLKEEASAMOADFOREALMAEFDPNPIVTKLLGAVCAVCKPMCLFEYM 658
Db 540 PTNDKMLVAVKALKDPLLA-ARKDFOREALLTNLQHEHIYKFGYCGDDGDLPLMVEYM 598
QY 659 AYGDLEFLRSMSPHTVCSLSHSDLSMRAOYSSPP-----PLSCAEOLCIAQOVAAGM 713
Db 599 KHGDLNKLRAHGPD-----AMILVDGQPROAKGELGSLQMLHIASQIASGM 645
QY 714 AYLSERKFVHRDLATRNCLVGENNVYKIDAFGLSRNITYSADYRYKANENDAIPIRMPPES 773
Db 646 VYLAQHFVHRDLATRNCLVGENNVYKIDAFGLSRNITYSADYRYKANENDAIPIRMPPES 705
QY 774 IFYRRTTESDVMAVYVLAWEISYGLQPYYGMAHEEVIYVRDGNILSCPENCPVELYN 833
Db 706 IMYKRFETSDVMSFGVILMEIFTYGRQPMFQSLNTEVIECTIGRVLERPVCPEKYEYD 765
QY 834 LMRCLMSKLPADRPSTSIHRILEM 859
Db 766 IMLGCCQREPOQLNKIKETKILHAL 791

```

## RESULT 13

```

A55178
neurotrophin receptor trkC precursor - human
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 18-Jun-1999
C:Accession: A55178
R:McGregor, L.M.; Baylín, S.B.; Griffin, C.A.; Hawkins, A.L.; Nelkin, B.D.
Genomics 22, 267-272, 1994
A:Title: Molecular cloning of the cDNA for human TrkC (NTRK3), chromosomal assignment, a
A:Reference number: A55178; MUID:95104834
A:Accession: A55178
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-825 <MCG>
A:Cross-references: GB:U05012; NID:g442389; PIDN:AAA75374.1; PID:g442390
C:Genetics:
A:Gene: GDB:NTRK3
A:Cross-references: GDB:127899; OMIM:191316
A:Map position: 15q24-15q25
C:Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glycopo
C:Keywords: alternative splicing; ATP; growth factor receptor
F:79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
F:104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
F:128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
F:151-162/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical <LR
F:536-817/Domain: protein kinase homology <KIN>
F:544-552/Region: protein kinase ATP-binding motif

```

```

Query Match 17.7%; Score 809.5; DB: 2; Length 825;
Best Local Similarity 26.1%; Pred. No. 2.2e-33;
Matches 252; Conservative 126; Mismatches 245; Indels 343; Gaps 36;
QY 6 NIPLVHI-----LTVAFSGTEKL-----PKAPVITTPLETVDAVVEE 43
Db 79 NITSIHINMMSLTHTLNAVDELYTGLOKLTIKNSGLASIQPRAPAKPHLRITVLSNR 138
QY 44 VATFWCAVESYPOPEISWTNRKLIKLPDTRYSIRENGQLITLISVED----- 91
Db 139 LTT-----LSM-----QLRFQTL-SLSRE-----IQLEQNFNFGSCDIRMM 171

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QY 92 -----SDPGIYCCYANNNGVGA-----VESCGLAQVKKKPKITRPPIVVKI 132
Db 172 QLMQEGEALNLSNOLYCIAD-----GSQLPLFRMINSQDL-----PEISVSHVLTJV 221
QY 133 IEGLKAVLPCTMGNPKPSVSWI-----KGDSPLENSRIAVLESQIRIHNQKEDAG-Q 187
Db 222 REGDNNAVITCGSGSLPDDWITVTGLQSLINTQNTNMTNVHAINTLVNAVISEDGFT 281
QY 188 YRCVAKNSLG-----TAY--SKYVKLEFEVFAIRLRAPE--SHNVFGSFTVLTCT 234
Db 282 LFCIAENVVGMSSNAVITYPPRVVSL-----EPRLRLHCIEF-----V 324
QY 235 ATGIPVPTIWIENGNAVSSGSI--QSVKDRYIDSLQLEFTRP-----GLYTCTATNK 287
Db 325 VRGNPPTLHMLNQGDLRSKTIHVEYQEGEISEGCLLE-NKPTHYNNNGNTYLLAKNP 383
QY 288 HGEKFTAKAAATISTAEWSKPKQDNKGCAQVRGEVCNVLAKDALVELNTSYADEEA 347
Db 384 LG-----TANQNTN-----GH-----FLKEPP--PEST 404
QY 348 QELLVHTAMNELKVSPVCPRAEALCNHIFQECSPGVVPTPIPCREYCLAVELFCA 407
Db 405 DNFI-----LFDVSP----- 415
QY 408 KEWLMEKTHRGLYRSEMILLVYKCSKLPMSHMDPTACARLPHLDYKNEKLTFRPMT 467
Db 416 -----TPPT 420
QY 468 -SSKPSVDIPPLPSSSSSFSVSPYSMTVYISMSFAIFVLTITLYCCRRRKQKN 526
Db 421 VTHKPEED-----TFGVSTAVGLAAACVILVAVLFWMINKYGRSKFGM 464
QY 527 K-----KRESAAVLT-----TLPSSELLDRLHPNM--YQRPILLNKLKLSLEY 570
Db 465 KGPVAVISGEEDSASPLHINHGITPSSL--DAGDVTAVIGMTRIPVLENPOYFRQGN 521
QY 571 -----FRNNIEYVRDICEGAFGVFOARAGCLPYEPFTVAVKMLKEEASAD 618
Db 522 NCHKPDITYVOHIKRDIKRLRELGEAGFAGKFTLAECTNLSTPKKMLVAVKALKDPLLA- 580
QY 619 MQADFOREALMAEFDPNPIVTKLLGAVCAVCKPMCLFEYMAVGDLEFLRSMSPHTVCSL 678
Db 581 ARKDFOREALLTNLQHEHIYKFGYCGDDGDLIMVEFYKHGDLNKLRAHGPN----- 635
QY 679 SHSDLSMRAOYSSPP-----PLSCAEOLCIAQOVAAGMAYLSERKFVHRDLATRNCLV 733
Db 636 -----AMILVDGQPROAKGELGSLQMLHIASQIASGMVYLAQHFVHRDLATRNCLV 687
QY 734 GENNVYKIDAFGLSRNITYSADYRYKANENDAIPIRMPPESIFYRRTTESDVMAVYVLM 793
Db 688 GANILVYKIDFGMSRDYSTDYRYKVGCHTMLPIRMPPESIMYKRFETSDVMSFGVILM 747
QY 794 EIFYSGLOPYYGMAHEEVIYVRDGNILSCPENCPVELYNIMRCLMSKLPADRPSTSIH 853
Db 748 EIFTYGRQPMFQSLNTEVIECTIGRVLERPVCPEKYEYDVLMCGMREPOQLNKIKET 807
QY 854 RILERM 859
Db 808 KILHAL 813

```

## RESULT 14

```

JC4593
Protein-tyrosine kinase-related receptor PTK7 precursor - human
N:Alternate names: receptor protein tyrosine kinase-like protein (RPTK)
C:Species: Homo sapiens (man)
C>Date: 16-Apr-1996 #sequence_revision 24-May-1996 #text_change 24-Sep-1999
C:Accession: JC4593
R:Park, S.K.; Lee, H.S.; Lee, S.T.
J. Biochem. 119, 235-239, 1996
A:Title: Characterization of the human full-length PTK7 cDNA encoding a receptor prot
A:Reference number: JC4593; MUID:97037064
A:Accession: JC4593

```

A: Molecule type: mRNA  
A: Residues: 1-1070 <PAB>  
A: Cross-references: GB:U04271; NID:91322231; PIDN:AAC0484.1; PID:91322232  
C: Comment: This protein is a member of receptor protein tyrosine kinase family, but prot  
C: Geneticks:  
A: Gene: GDB: PTK7  
A: Cross-references: GDB:134760; OMIM:601890  
A: Map position: 6p21.1-6p12.2  
C: Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo  
C: Keywords: cell adhesion; extracellular protein; glycoprotein; phosphotransferase; tran  
F: 1-30/Domain: signal sequence #status predicted <SIG>  
F: 31-1070/Product: protein-tyrosine kinase 7 #status predicted <MAT>  
F: 31-703/Domain: extracellular #status predicted <EXT>  
F: 704-725/Domain: transmembrane #status predicted <TM>  
F: 726-1070/Domain: intracellular #status predicted <INC>  
F: 794-1065/Domain: protein kinase homology <KIN>  
F: 116,175,184,214,268,283,405,463,567,646/Binding site: carbohydrate (Asn) (covalent) #

Query Match 17.4%; Score 793; DB 2; Length 1070;  
Best Local Similarity 27.8%; Pred. No. 1.9e-32;  
Matches 233; Conservative 136; Mismatches 300; Indels 168; Gaps 30;

QY 55 POPELSMTNRKILIKLFDTRYSIRENGQLITLVEDSDGICYCTANNVCGAVESGCA 114  
DB 330 PEPSSVMMHAGVRL--PTGHRVYQKGHELVYLANIAESDAGVYTHAANLACQRQDVN- 405  
QY 115 LQVKKPKITRPPINVKIIEGLKAVLPCTTMGNPKPSVSMIGSDSPLRNSRIAVLESQS 174  
DB 406 ITVAIVPSPMVKKPODSOLEGKPGYLDLTQATPKPTVYVYRNOMLISDSFEVFKNGT 465  
QY 175 LRINAVQKEDAGQYRCVAKNSLGT--AVSKVYKLEFEVFAIRLAPESHN-VTFGSEVYL 231  
DB 466 LRINSVEYDDGTWYRCMSSTPAGSIEAQRVYLEKFT--PPQPOQCEFEFKKATV 522  
QY 232 HCTAIGIVPTITWENGNVSSGSIQSVKDRVIDSLQLEFTR-----PELYCIATN 286  
DB 523 PCSATGKREKPTIKWR-----ADGS--SLPEWYDNGTGFHFAVYRDDAGNYICISN 574  
QY 287 KHGEKSTAKAAATISIAEWSKPOKDNKGYCAQYGEVCNVAKLADALVFLNTSYADPEE 346  
DB 575 -----GPOGQIRAHVQLVY-----AVFI-TFKEVEPR 600  
QY 347 AOELLVHTANMELKVVSYVCPRAEALCNHIFQCSGCVVPTPIPIREYCLAVKELFC 406  
DB 601 TTVYOGHTA-----LLOCEAQGDPKPL----- 622  
QY 407 AKEWLVMEKTRHGLYRSEHMLSVKCSKLPMSH-----WDPTACARLPHTDY 455  
DB 623 -IQW-----KKDKILDPRTKLG--PRNHIFQNGSLVHDVAPEDSGRTTCIAG 667  
QY 456 NKEMLK-TFPPMTSSKPSVDIPNLPSSSSSSFVSPTYSM--TVIISIMSSFPIVLLTI 512  
DB 668 NSCNKIKHTEAPLY---VVDKP-VPSESEPGGS-PPPYKMIQTIGLSVGAANAIVAVLG 721  
QY 513 TTLVC---CRRRQWKNNKKRESAAVTL-----TLLPSELLDRLHPNMYRM 557  
DB 722 LMFCKCKRCKKRILOKQEGEPEMECLNGPRLONGOPSAEIOEVALTISGSGPAATNK 781  
QY 558 PLLNPKLLSEYRNNIEYVRDIEGAFGRVFOARAPGLPYEPFTVAVKMLKEESA 617  
DB 782 RHSTSDK---MHPFRSSLOPITTLGKSEFGEVFLAKAGLEGAETLVLKSLQTK-DE 837  
QY 618 DMQADFOREALMAEFQNPVYKLLGCAVAGKPMCLFEYVAGDNLNFEFLSMSPHYCS 677  
DB 838 QQQQLDFRRELEMEGLNLIANVYRLGLCREAPHYMYLEVYDLDLKQFLR----- 888  
QY 678 LSHS-DLSRAQVSSPPPLSCAEOLCIAROVAAGMAVYSEFVHDLTRNCTIAGEN 736  
DB 889 ISKSKDELKQ-----PLSTKQKVALCTQVALGHEHLSNNRPFVKHDLARAKMLSAQ 941  
QY 737 MVVYIADFGLSRNITYSADYKANENDALPIRMMPESITFYRNYTESDVNAVYGVLEIF 796  
DB -----

DB 942 RQVKSALGLSKDQVNSEYHFERO-AMVPLRWMSPAILLEGDRSTKSDVWAFGLMMEYF 1000  
QY 797 SYGLQRYQYMAHDEVIYYRRDGNH-LSCPENGCEVELYNLMRLCWSKLPADRPSTFI 852  
DB 1001 THEEMPHGQADDEVLIADLQAGAKARLPQEGCGSKLYRLMQRWALSPXDRPSFSEI 1057

RESULT 15  
173632  
neurotrophin-3 receptor precursor - human  
N: Alternate names: receptor tyrosine kinase trkC  
N: Contains: protein-tyrosine kinase (EC 2.7.1.112)  
C: Species: Homo sapiens (man)  
C: Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 11-Jun-1999  
R: Shetton, D.L.; Sutherland, J.; Gripp, J.; Camerato, T.; Armanini, M.P.; Phillips, H.  
J. Neurosci. 15, 477-491, 1995  
A: Title: Human trks: molecular cloning, tissue distribution, and expression of extrac  
A: Reference number: 156557; MUID:95123473  
A: Accession: 173632  
A: Status: preliminary; translated from GB/EMBL/DBJ  
A: Molecule type: mRNA  
A: Residues: 1-839 <RES>  
A: Cross-references: GB:S76475; NID:9913721; PIDN:AAB33111.1; PID:9913722  
C: Geneticks:  
A: Gene: GDB: NTRK3; TRKC  
A: Cross-references: GDB:1278999; OMIM:191316  
A: Map position: 15q24-15q25  
C: Function:  
A: Description: regulation of nervous system development; receptor for neurotrophin-3  
C: Superfamily: nerve growth factor receptor, high affinity; leucine-rich alpha-2-glyc  
C: Keywords: ATP; autophosphorylation; brain; glycoprotein; growth factor receptor; ph  
F: 1-31/Domain: signal sequence #status predicted <SIG>  
F: 32-839/Product: neurotrophin-3 receptor #status predicted <MAT>  
F: 32-436/Domain: extracellular #status predicted <EXT>  
F: 79-103/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR1>  
F: 104-127/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR2>  
F: 128-150/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LR3>  
F: 151-162/Domain: leucine-rich alpha-2-glycoprotein repeat homology #status atypical  
F: 437-453/Domain: transmembrane #status predicted <TM>  
F: 454-839/Domain: cytosolic #status predicted <CT>  
F: 536-831/Domain: protein kinase homology <KIN>  
F: 544-552/Region: protein kinase ATP-binding motif  
F: 72,79,133,163,203,218,232,259,267,294,375,388/Binding site: carbohydrate (Asn)  
F: 572/Active site: Lys #status predicted  
F: 709/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predi  
F: 834/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 17.3%; Score 792.5; DB 1; Length 839;  
Best Local Similarity 25.9%; Pred. No. 1.6e-32;  
Matches 254; Conservative 125; Mismatches 244; Indels 357; Gaps 38;

QY 6 NIPLVHI-----LTLVAFSGTERKL-----PKAVITTPLETVALVEE 43  
DB 79 NITSIHENMNSLHTLANVDMELYGLQKLTIKNSGLNSIOPRAAKNPHLETYINLSNR 138  
QY 44 VATEMCAYESYPOPEISWTRNKKILIKLFDTRYSIRENGQLITLVED----- 91  
DB 139 LTT-----LSW-----QLFQT-LSLRE-----LOLEONFENGSCDIRM 171  
QY 92 -----SDGICYCTANNVCGA-----VESCGLQVKKMKPKITRPPINVKI 132  
DB 172 QLMQDQGEAKINSOMLYCIND---GSOLPLFRNNIQCDL-----PEISVSHVNTLV 221  
QY 133 IEGLKAVLPCTTMGNPKPSVSMI-----KGDSPLRNSRIAVLESGLRIHVQKQDAG-Q 187  
DB 222 REGDNAVITTCNGSGSPPLDVVITYTGLOSTINRQTNLMWTVNHAINTLVAVTSDNQFT 281  
QY 188 YRCVAKNSLG-----TAY--SKVYKLEFEVFAIRLAPB---SHNVTFGSEFVTLHCT 234  
DB 282 LTGIAENVVGMSNVSVALTYVYPRVVSLE-----EDELRLHEHIEF-----V 324



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 16, 2002, 13:36:00 ; Search time 37.92 Seconds

(without alignments)  
3964.467 Million cell updates/sec

Title: US-09-817-487a-2

Perfect score: 4569

Sequence: 1 MRELVINIPVHILTLVAFSG.....TSIHRIILERMOCERAGTIVSV 869

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL\_19:\*

1: sp\_archaea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_mhc:\*

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_protist:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriophage:\*

17: sp\_archae:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4558	99.8	869	4	015146
2	4282.5	93.9	868	11	062838
3	4269.5	93.4	868	11	061006
4	4220.5	92.4	860	11	061005
5	4136	90.5	871	11	061987
6	4128	90.3	881	11	061988
7	2897	63.4	946	13	007153
8	1602	35.1	354	13	09DDA2
9	1129.5	24.7	724	5	09V6K3
10	966.5	21.2	1145	5	09BKL8
11	802	17.6	821	13	09YH44
12	801	17.5	811	13	09YH43
13	792.5	17.3	839	4	075682
14	778	17.0	865	5	024488
15	773.5	16.9	928	5	09BLV1
16	772	16.9	902	5	017576

17	754.5	16.5	591	4	015656	015656 homo sapien
18	750.5	16.4	790	13	090699	090699 gallus gall
19	740.5	16.2	503	4	015655	015655 homo sapien
20	738.5	16.2	486	13	09PST9	09PST9 xenopus lae
21	724.5	15.9	802	13	042127	042127 xenopus lae
22	720	15.8	782	13	061563	061563 mus musculu
23	720	15.8	796	13	021287	021287 pleurodeles
24	720	15.8	972	5	026614	026614 strongyloce
25	715	15.6	800	4	099052	099052 homo sapien
26	712	15.5	282	13	091373	091373 xenopus. tr
27	709	15.5	800	11	09JHX9	09JHX9 rattus norv
28	708	15.5	922	13	090413	090413 brachydanio
29	705.5	15.4	814	13	091887	091887 xenopus lae
30	702.5	15.4	802	6	095M13	095M13 bos taurus
31	697.5	15.3	650	11	063709	063709 rattus rat
32	696.5	15.2	810	13	09PS96	09PS96 xenopus lae
33	695.5	15.2	800	13	0918X3	0918X3 brachydanio
34	690.5	15.1	989	13	09PMW6	09PMW6 gallus gall
35	686.5	15.0	824	13	090749	090749 gallus gall
36	681	14.9	766	4	096KM2	096KM2 homo sapien
37	681	14.9	785	4	096KM1	096KM1 homo sapien
38	681	14.9	819	4	096KM0	096KM0 homo sapien
39	679	14.9	822	11	060818	060818 mus musculu
40	677	14.8	876	11	060752	060752 mus musculu
41	676	14.8	782	6	09RTZ3	09RTZ3 oryctolagus
42	676	14.8	806	13	090Z00	090Z00 brachydanio
43	671	14.7	609	13	091776	091776 xenopus lae
44	670	14.7	1358	13	073798	073798 xenopus lae
45	670	14.7	1362	13	09PVZ4	09PVZ4 xenopus lae

## ALIGNMENTS

RESULT 1

ID 015146 PRELIMINARY: PRT: 869 AA.

AC 015146;

DT 01-JAN-1998 (TREMBLrel. 05. Created)

DT 01-JAN-1998 (TREMBLrel. 05. Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19. Last annotation update)

DE MUSCLE SPECIFIC TYROSINE KINASE RECEPTOR.

GN MUSK.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96009854; PubMed=7546737;

RA Valenzuela D.M., Stitt T.N., Disfano P.S., Rojas E., Mattsson K.,

RA Compton D.L., Nunez L., Park J.S., Stark J.L., Giles D.R., Thomas S.,

RA LeBeau M.M., Fernald A.A., Copeland N.G., Jenkins N.A., Buden S.J.,

RA Glass D.J., Yancopoulos G.D.;

RT "Receptor tyrosine kinase specific for the skeletal muscle lineage: expression in embryonic muscle, at the neuromuscular junction, and after injury.";

RT Neuron 15:573-584 (1995).

[2]

SEQUENCE FROM N.A.

RA Valenzuela D.M., Rojas E., Yancopoulos G.D.;

RA Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

RL EMBL: AF006464; AAB63044.1; -

DR HSSP: P11362; IFGK.

DR InterPro: IPR002453; Beta.tubulin.

DR InterPro: IPR000719; Btk-Dkinase.

DR InterPro: IPR000024; Fz-domain.

DR InterPro: IPR003598; Ig\_c2.

DR InterPro: IPR003006; Ig\_MHC.

DR Pfam: PF01392; Fz; 1.

DR Pfam: PF00047; Ig; 3.

DR Pfam: PF00069; pkinase; 1.

PRINTS: PRO0109; TYRKINASE.  
 DR SMART; SM00408; IGC2; 3.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS00038; FZ; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00228; TUBULIN\_B\_AUTOREG; 1.  
 DR PROSITE; PS00228; TUBULIN\_B\_AUTOREG; 1.  
 DR ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;  
 KW Tyrosine-protein kinase.  
 SO SEQUENCE 869 AA; 97056 MW; 3DDC20E179FA010C CRC64;

Query Match 99.8%; Score 4558; DB 4; Length 869;  
 Best Local Similarity 99.8%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;  
 Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRELVINPIVLHILTLVAFSGTEKLPKAPVITTPLETVDALVEEVAATFMCVAVESYPOPEIS 60  
 DB 1 MRELVINPIVLHILTLVAFSGTEKLPKAPVITTPLETVDALVEEVAATFMCVAVESYPOPEIS 60  
 Y 61 WTRNKILIKLFDTRYSTRIRNGQLTITLISVEDSDGIYCCCTANNVGAVESGALQYKMK 120  
 DB 61 WTRNKILIKLFDTRYSTRIRNGQLTITLISVEDSDGIYCCCTANNVGAVESGALQYKMK 120  
 QY 121 PKITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGDSPLRENSRIAVLESGLRIHNV 180  
 DB 121 PKITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGDSPLRENSRIAVLESGLRIHNV 180  
 QY 181 OKEDAGQRCVAKNSLGTAVSKVYKLEFEVAPARILRAPESHNVTFGSFVTLHCTATGIPV 240  
 DB 181 OKEDAGQRCVAKNSLGTAVSKVYKLEFEVAPARILRAPESHNVTFGSFVTLHCTATGIPV 240  
 QY 241 PPTIWIINGNAVSSGSIOESYKDVDSRLQIFTFKPGLTCTATNKGHEKSTAKAAAT 300  
 DB 241 PPTIWIINGNAVSSGSIOESYKDVDSRLQIFTFKPGLTCTATNKGHEKSTAKAAAT 300  
 QY 301 ISIAEMSKPOKDNKGCAQYRGECVNAVLAKDALVPLNTSYADEEAOELLVHTAMNELK 360  
 DB 301 ISIAEMSKPOKDNKGCAQYRGECVNAVLAKDALVPLNTSYADEEAOELLVHTAMNELK 360  
 QY 361 VVSVCPRPAEALCNHIFECSPGVVPTPIPCIREYCLAVKELFCAKEMLVMEKTHRG 420  
 DB 361 VVSVCPRPAEALCNHIFECSPGVVPTPIPCIREYCLAVKELFCAKEMLVMEKTHRG 420  
 QY 421 LYREEMHLSPKCSKLPMSHMDPTACARPLHDYKNENKTFPPMSSSKSVDPINLPS 480  
 DB 421 LYREEMHLSPKCSKLPMSHMDPTACARPLHDYKNENKTFPPMSSSKSVDPINLPS 480  
 QY 481 SSSSSFSVPTYSMTVIISIMSSFAIFVLTITTLTYCCRRKKQKMKKRESAAVTLTLP 540  
 DB 481 SSSSSFSVPTYSMTVIISIMSSFAIFVLTITTLTYCCRRKKQKMKKRESAAVTLTLP 540  
 QY 541 SELLDRLHPPMPQORPILNPKLISLEVRNNIEYVROIGEGAFGVPPARAPGLIPY 600  
 DB 541 SELLDRLHPPMPQORPILNPKLISLEVRNNIEYVROIGEGAFGVPPARAPGLIPY 600  
 QY 601 EPTFMVAVKMLKEBASADMDQFORREALMAEFDNPNIIVKLIGYCAVKGPKCLLFYWAY 660  
 DB 601 EPTFMVAVKMLKEBASADMDQFORREALMAEFDNPNIIVKLIGYCAVKGPKCLLFYWAY 660  
 QY 661 GDLNEFLKMSPTVCSLSHSDLSMRAOVSSPPPLSCAQDLICAROVAAGMAYLSERK 720  
 DB 661 GDLNEFLKMSPTVCSLSHSDLSMRAOVSSPPPLSCAQDLICAROVAAGMAYLSERK 720  
 QY 721 FVHNDLATRNCLVGENMVAKTADFGLSNITYSADYKANENDAPIRMPPESTIFYNYT 780  
 DB 721 FVHNDLATRNCLVGENMVAKTADFGLSNITYSADYKANENDAPIRMPPESTIFYNYT 780  
 QY 781 TESDVAAGVVLMEIFSYGLQPYGMAHEEVIYVRDGNILSCPENCPVELLYNMLRLCWS 840  
 DB 781 TESDVAAGVVLMEIFSYGLQPYGMAHEEVIYVRDGNILSCPENCPVELLYNMLRLCWS 840

QY 841 KLPADRPSTSIHRLIEMRCERAGTVSV 869  
 DB 841 KLPADRPSTSIHRLIEMRCERAGTVSV 869

RESULT 2  
 ID 062838 PRELIMINARY; PRT: 868 AA.  
 AC 062838;  
 DT 01-NOV-1996 (TRENBLREL. 01, Created)  
 DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)  
 DE MUSCLE-SPECIFIC TYROSINE KINASE RECEPTOR MUSK.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96009854; PubMed=7546737;  
 RA Valenzuela D.M., Stilt T.N., Distefano P.S., Rojas E., Mattsson K.,  
 RA Compton D.L., Nunez L., Park J.S., Stark J.L., Gies D.R., Thomas S.,  
 RA Lebeau M.M., Fernald A.A., Copeland N.G., Jenkins N.A., Burden S.J.,  
 RA Glass D.J., Yancopoulos G.D.;  
 RT "Receptor tyrosine kinase specific for the skeletal muscle lineage:  
 RT expression in embryonic muscle, at the neuromuscular junction, and  
 RT after injury.";  
 RL Neuron 15:573-584(1995).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL: U34985; AAA0956.1; -.  
 DR HSSP: P13362; 1EGK  
 DR InterPro: IPR002453; Beta\_tubulin.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000024; Fz\_domain.  
 DR InterPro: IPR003598; Ig\_c2.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF01392; Fz; 1.  
 DR Pfam: PF00047; Ig; 3.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PRO0109; TYRKINASE.  
 DR SMART: SM00408; IGC2; 3.  
 DR SMART: SM00219; TYRK; 1.  
 DR PROSITE; PS00038; FZ; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00101; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS00228; TUBULIN\_B\_AUTOREG; 1.  
 DR ATP-binding; Immunoglobulin domain; Kinase; Receptor;  
 KW Serine/threonine-protein kinase; Transferase.  
 SO SEQUENCE 868 AA; 96821 MW; C146B4E74EE25B24 CRC64;

Query Match 93.9%; Score 4292.5; DB 11; Length 868;  
 Best Local Similarity 93.2%; Pred. No. 0; Mismatches 27; Indels 1; Gaps 1;  
 Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

QY 1 MRELVINPIVLHILTLVAFSGTEKLPKAPVITTPLETVDALVEEVAATFMCVAVESYPOPEIS 60  
 DB 1 MRELVINPIVLHILTLVAFSGTEKLPKAPVITTPLETVDALVEEVAATFMCVAVESYPOPEIS 60  
 QY 61 WTRNKILIKLFDTRYSTRIRNGQLTITLISVEDSDGIYCCCTANNVGAVESGALQYKMK 120  
 DB 61 WTRNKILIKLFDTRYSTRIRNGQLTITLISVEDSDGIYCCCTANNVGAVESGALQYKMK 120  
 QY 121 PKITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGDSPLRENSRIAVLESGLRIHNV 180  
 DB 121 PKITRPPINVKIIEGLKAVLPCTTMGNPKPSVSWIKGDSPLRENSRIAVLESGLRIHNV 180  
 QY 181 OKEDAGQRCVAKNSLGTAVSKVYKLEFEVAPARILRAPESHNVTFGSFVTLHCTATGIPV 240  
 DB 181 OKEDAGQRCVAKNSLGTAVSKVYKLEFEVAPARILRAPESHNVTFGSFVTLHCTATGIPV 240

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Db 181 OKEDAGYRCVANKSLGTAYSKLVKLEVEFARILRAPESHNTFGSFYTLRCTAIGMPV 240
QY 241 PTTWTIENGNAVSSGSIQSVKDRVIDSRLOLFTPKGYLTCTATNKHGEKSTAKAAAT 300
Db 241 PTTWTIENGNAVSSGSIQSVKDRVIDSRLOLFTPKGYLTCTATNKHGEKSTAKAAAT 300
QY 301 ISIAEWSKQKDNKGCAOYRGEVCNAVLAKDALVFLNTSYADPEBAQELLVHTANNEK 360
Db 301 ISIAEWSKQKDNKGCAOYRGEVCNAVLAKDALVFLNTSYADPEBAQELLVHTANNEK 360
QY 361 VSPICRPAEALLCNHLHFOECSPGVPTPIPCREYCLAWEKLFCAKEKLMVEETHNG 420
Db 361 VSPICRPAEALLCNHLHFOECSPGVPTPIPCREYCLAWEKLFCAKEKLMVEETHNG 420
QY 421 LYRSEMHLLSVKCSKLPMSHMDPTACARLPHLDYKNEKLTFFPMTSSKPSVDINLPS 480
Db 421 LYRSEMHLLSVKCSKLPMSHMDPTACARLPHLDYKNEKLTFFPMTSSKPSVDINLPS 480
QY 481 SSSSSFSVSPYVSMYIISIMSSFAIFVLLTTTLYCCRRRQWKKKRESAAVLTTLTP 540
Db 480 ASTSFVAVSPAYSMYIISIMSCFAVFAVLLTTTLYCCRRRREKKKKRESAAVLTTLTP 539
QY 541 SELLDRILHPNMYOQMPLLNPKLLSTLEYPRNNIEYVNDIGEGARGVFOAARAPGLPY 600
Db 540 SELLDRILHPNMYOQMPLLNPKLLSTLEYPRNNIEYVNDIGEGARGVFOAARAPGLPY 599
QY 601 EPTTVAVAMKLEASADQADFORAALMAEFENDNITKLGVCVAVGKPMCLLFETMAY 660
Db 600 EPTTVAVAMKLEASADQADFORAALMAEFENDNITKLGVCVAVGKPMCLLFETMAY 659
QY 661 GDLNEFLRSMSPHTVCSLSHSDLSMRQOVSFSGPPPLSCAEOLCIAROYAAGMAYLSERK 720
Db 660 GDLNEFLRSMSPHTVCSLSHSDLSMRQOVSFSGPPPLSCAEOLCIAROYAAGMAYLSERK 719
QY 721 FVHRDLATNCLVGENMYVKIADFGLSRNIYSADYKKAENOAIPTRMMPPEISFYNNRT 780
Db 720 FVHRDLATNCLVGENMYVKIADFGLSRNIYSADYKKAENOAIPTRMMPPEISFYNNRT 779
QY 781 TESDWAYGVVLMELFYSGLQPYGYMAHEVITYYVADGNILSCPENCPVELYNLMRLCS 840
Db 780 TESDWAYGVVLMELFYSGLQPYGYMAHEVITYYVADGNILACBPENCPVELYNLMRLCS 839
QY 841 KLPADRPSTSTHRLIERMCEBEGVSY 869
Db 840 KLPADRPSTSTHRLIERMCEBEGVSY 868

RESULT 3
ID 061006 PRELIMINARY: PRT: 868 AA.
AC 061006:
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MUSCLE LOCALIZED KINASE 2.
OS Mus musculus (Mouse).
OC Euteleostomi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Caruso A., Morris J.C., Neben S., Flinnerly H., Beler D., Turner K.,
RA Wood C.R.;
RL Submitted (OCT-1995) to the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: U37709; AAA79204.1; -.
DR HSSP: P11362; IFGK
DR InterPro: IPR002453; Beta_tubulin.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR003598; Iq_c2.
DR InterPro: IPR003006; Iq_MHC.
DR InterPro: IPR002290; Ser_thr_kinase.

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DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF01392; Fz_1.
DR Pfam: PF00047; Iq_3.
DR Pfam: PF00069; pkinase_1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00408; IGC2_3.
DR SMART: SM00219; TYRK_1.
DR PROSITE: PS00038; Fz_1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM_1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST_1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
DR PROSITE: PS00228; TUBULIN_B_AUTOREG_1.
KW ATP-binding; Immunoglobulin domain; kinase;
KW Serine/threonine-protein kinase; Transferase;
SQ SEQUENCE 868 AA; 96692 MW; AFE4E644C6869933 CRC64;

Query Match 93.4%; Score 4269.5; DB 11; Length 868;
Best local similarity 92.9%; Pred. No. 0;
Matches 807; Conservative 30; Mismatches 31; Indels 1; Gaps 1;

QY 1 MRELVIPIVHLITLVAFGSTKLPKAPVITTPLETVDAVBEVATPMCAVESYPOPEIS 60
Db 1 MRELVIPIVHLITLVAFGSTKLPKAPVITTPLETVDAVBEVATPMCAVESYPOPEIS 60
QY 61 WTRNKLLILFDTRYISIRENGQLTLISVEDSDGITYCCANNGVAGVESCAGALQVKK 120
Db 61 WTRNKLLILFDTRYISIRENGQLTLISVEDSDGITYCCANNGVAGVESCAGALQVKK 120
QY 121 PKTRPPINVKIIEGLKAVLPCTTMGNPPRSVSWIKGSDPLRNSRIAVLESGLRIHNV 180
Db 121 PKTRPPINVKIIEGLKAVLPCTTMGNPPRSVSWIKGSDPLRNSRIAVLESGLRIHNV 180
QY 181 OKEDAGYRCVANKSLGTAYSKLVKLEVEFARILRAPESHNTFGSFYTLRCTAIGIPV 240
Db 181 OKEDAGYRCVANKSLGTAYSKLVKLEVEFARILRAPESHNTFGSFYTLRCTAIGIPV 240
QY 241 PTTWTIENGNAVSSGSIQSVKDRVIDSRLOLFTPKGYLTCTATNKHGEKSTAKAAAT 300
Db 241 PTTWTIENGNAVSSGSIQSVKDRVIDSRLOLFTPKGYLTCTATNKHGEKSTAKAAAT 300
QY 301 ISIAEWSKQKDNKGCAOYRGEVCNAVLAKDALVFLNTSYADPEBAQELLVHTANNEK 360
Db 301 ISIAEWSKQKDNKGCAOYRGEVCNAVLAKDALVFLNTSYADPEBAQELLVHTANNEK 360
QY 361 VSPICRPAEALLCNHLHFOECSPGVPTPIPCREYCLAWEKLFCAKEKLMVEETHNG 420
Db 361 VSPICRPAEALLCNHLHFOECSPGVPTPIPCREYCLAWEKLFCAKEKLMVEETHNG 420
QY 421 LYRSEMHLLSVKCSKLPMSHMDPTACARLPHLDYKNEKLTFFPMTSSKPSVDINLPS 480
Db 421 LYRSEMHLLSVKCSKLPMSHMDPTACARLPHLDYKNEKLTFFPMTSSKPSVDINLPS 479
QY 481 SSSSSFSVSPYVSMYIISIMSSFAIFVLLTTTLYCCRRRQWKKKRESAAVLTTLTP 540
Db 480 ASTSFVAVSPAYSMYIISIVSFAIFVLLTTTLYCCRRRREKKKKRESAAVLTTLTP 539
QY 541 SELLDRILHPNMYOQMPLLNPKLLSTLEYPRNNIEYVNDIGEGARGVFOAARAPGLPY 600
Db 540 SELLDRILHPNMYOQMPLLNPKLLSTLEYPRNNIEYVNDIGEGARGVFOAARAPGLPY 599
QY 601 EPTTVAVAMKLEASADQADFORAALMAEFENDNITKLGVCVAVGKPMCLLFETMAY 660
Db 600 EPTTVAVAMKLEASADQADFORAALMAEFENDNITKLGVCVAVGKPMCLLFETMAY 659
QY 661 GDLNEFLRSMSPHTVCSLSHSDLSMRQOVSFSGPPPLSCAEOLCIAROYAAGMAYLSERK 720
Db 660 GDLNEFLRSMSPHTVCSLSHSDLSMRQOVSFSGPPPLSCAEOLCIAROYAAGMAYLSERK 719
QY 721 FVHRDLATNCLVGENMYVKIADFGLSRNIYSADYKKAENOAIPTRMMPPEISFYNNRT 780
Db 720 FVHRDLATNCLVGENMYVKIADFGLSRNIYSADYKKAENOAIPTRMMPPEISFYNNRT 779

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QY 781 TESDVMAAGVYLVMEIFSYGLQPYGYMAHEEYIYVRDGNILSCPCNPVELYINMLRCLWS 840
DB 780 TESDVMAAGVYLVMEIFSYGLQPYGYMAHEEYIYVRDGNILSCPCNPVELYINMLRCLWS 839
QY 841 KLPADRPSTSIHRIILERMCEAEGTVSV 869
DB 840 KLPADRPSTSIHRIILERMCEAEGTVGV 868

RESULT 4
ID 061005 PRELIMINARY; PRT; 860 AA.
AC 061005;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MOSCLE LOCALIZED KINASE 1.
GN MKI1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
BX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Caruso A., Morris J.C., Neben S., Finnerty H., Belier D., Turner K.,
RA Wood C.R.;
RT Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: U37708; AAA79203.1; -.
DR HSSP: P11362; IFGK.
DR InterPro: IPR002453; Beta_tubulin.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003066; Ig_MHC.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF01392; \Fz; 1.
DR Pfam: PF00047; \Fz; 3.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00408; IGC2; 3.
DR SMART: SM00219; TYRKc; 1.
DR PROSITE: PS50038; FZ; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00228; TUBULIN_B_AUTOREG; 1.
DR APP-binding: Immunoglobulin domain; Kinase; Transferase;
KW Tyrosine-protein kinase.
KW SEQUENCE 860 AA; 95670 MW; A837F8299BD7494C CRC64;
2

Query Match 92.4%; Score 4220.5; DB 11; Length 860;
Best Local Similarity 92.2%; Pred. No. 0;
Matches 801; Conservative 29; Mismatches 30; Indels 9; Gaps 2;

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DB 241 PTIWIENGNAVSSGSIOESVKDVRIDSRQLFTTKRGLYCIATNNHGEFSTAKAAT 300
QY 301 ISIEMWSPKDNKGCAOYAGEVCNMAVLAKDALVFLTSVADEDEAOELLVHTANNEIK 360
DB 301 ISIEMWSPKDNKGCAOYAGEVCNMAVLAKDALVFLTSVADEDEAOELLVHTANNEIK 360
QY 361 VSPVCRPAEALCNHIFQCSGPGVYPTPIPIGECYCLAVKELFCAKEWLMEEKTHRG 420
DB 361 AVSPLCRPAEALCNHIFQCSGPGVYPTPIPIGECYCLAVKELFCAKEWLMEEKTHRG 420
QY 421 LYRSEMHLLSPKCSKLPMSHMDPTACARLPHLDYKNENLTPPMNKSRSVDLPNLS 480
DB 421 LYRSGMHLLPYECSKLPMSHMDPTACTRLPYL-----AFPSITSSRSADLPNLP- 471
QY 481 SSSSFSPSPYSMTVIISIMSFATFLLTITLLCCRRKQMKKRESAAVTITLLP 540
DB 472 ASISSFAVSPYSMTVIISIVSFPALRALTLATLYCCRKKEMKKNKRESTATVITLLP 531
QY 541 SELLDRLHPNMQRMPLLNPKLLSLEYPRNNIEYVRDIGEGAFGRVQARAPGLLPY 600
DB 532 SELLDRLHPNMQRMPLLNPKLLSLEYPRNNIEYVRDIGEGAFGRVQARAPGLLPY 591
QY 601 EPTTMVAVKMLKEASADMDQDFOREAALMAEFDPNPVYKLLGCAVCKPKCLLFEYVAY 660
DB 592 EPTTMVAVKMLKEASADMDQDFOREAALMAEFDPNPVYKLLGCAVCKPKCLLFEYVAY 651
QY 661 GDNLNPLRSMSPHYVCSLSHSDLSMRAQVSSPGPPSLCAQOLCIAROVAAGMAYLSERK 720
DB 652 GDNLNPLRSMSPHYVCSLSHSDLSMRAQVSSPGPPSLCAQOLCIAROVAAGMAYLSERK 711
QY 721 FVHRDLATRNCLVGENMYVKTADFGLSRNYSADYKANENDAIPIRMPPESIFYNRYT 780
DB 712 FVHRDLATRNCLVGENMYVKTADFGLSRNYSADYKANENDAIPIRMPPESIFYNRYT 771
QY 781 TESDVMAAGVYLVMEIFSYGLQPYGYMAHEEYIYVRDGNILSCPCNPVELYINMLRCLWS 840
DB 772 TESDVMAAGVYLVMEIFSYGLQPYGYMAHEEYIYVRDGNILSCPCNPVELYINMLRCLWS 831
QY 841 KLPADRPSTSIHRIILERMCEAEGTVSV 869
DB 832 KLPADRPSTSIHRIILERMCEAEGTVGV 860

RESULT 5
ID 061987 PRELIMINARY; PRT; 871 AA.
AC 061987;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE NSK2 PROTEIN PRECURSOR.
GN MUSK OR NSK2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
BX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=MYOBLAST;
RC MEDLINE=95349951; PubMed=7624144;
RX Ganju P., Walls E., Brennan J., Reich A.D.;
RA "Cloning and developmental expression of Nsk2, a novel receptor
RT tyrosine kinase implicated in skeletal myogenesis...";
RL OncoGene 11:281-290(1995).
CC 1-1 SIMILARITY: BELONGS TO THE SBR/THR FAMILY OF PROTEIN KINASES.
DR EMBL: X86444; CA60165.1; -.
DR HSSP: P11362; IFGK.
DR MGD; MGI:103581; Musk.
DR InterPro: IPR002453; Beta_tubulin.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR003598; Ig_c2.

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DR InterPro: IPR003600; Ig-like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR002290; Ser\_thr\_kinase.  
DR InterPro: IPR001245; Tyr\_kinase.  
DR Pfam: PF01392; Fz; 1.  
DR Pfam: PF00047; Ig; 3.  
DR Pfam: PF00069; kinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR SMART: SM00408; IGC2; 2.  
DR SMART: SM00410; IG-like; 1.  
DR SMART: SM00219; Tyrc; 1.  
DR PROSITE: PS50038; Fz; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE: PS00228; TUBULIN\_B\_AUTOREG; 1.  
DR ATP-binding; Immunoglobulin domain; Serine/threonine-protein kinase;  
KW Signal; Transferase.  
FT SIGNAL 1  
SQ SEQUENCE 871 AA; 97047 MW; F3C53DC6AFE702AB CRC64;

Query Match 90.5%; Score 4136; DB 11; Length 871;

Best Local Similarity 90.3%; Pred. No. 0;

Matches 790; Conservative 30; Mismatches 45; Indels 10; Gaps 4;

QY 1 MRELVINPVLHIITLVAFGSTETKLPKAPVITTPLETVDAIVEVATFMCVESTPOPEIS 60  
DB 1 MRELVINPVLHIITLVAFGSTETKLPKAPVITTPLETVDAIVEVATFMCVESTPOPEIS 60  
QY 61 WTRNKLILKLPDTRYSIRENGQLLTLLSYEDSDGTYCCTANNVGAVESGALOVKMK 120  
DB 61 WTRNKLILKLPDTRYSIRENGQLLTLLSYEDSDGTYCCTANNVGAVESGALOVKMK 120  
QY 121 PRTTRPPIVVKIIEGKAVLPCTTGNPKPSVWIKGDSPLRENSKRAVESSSLRIHNY 180  
DB 121 PRTTRPPIVVKIIEGKAVLPCTTGNPKPSVWIKGDSPLRENSKRAVESSSLRIHNY 180  
QY 181 OKEDAGQYRCVAKNSLGTATYSKVVKLEFEYFARILRAPESHNTFCSFVTLHCTATGIPV 240  
DB 181 OKEDAGQYRCVAKNSLGTATYSKVVKLEFEYFARILRAPESHNTFCSFVTLHCTATGIPV 240  
QY 241 PRTTWIENGNAVSSGSIQSVKDRVIDSRQLQFTFPGTYCTIATNKGKESFSTANAAT 300  
DB 241 PRTTWIENGNAVSSGSIQSVKDRVIDSRQLQFTFPGTYCTIATNKGKESFSTANAAT 300  
QY 301 ISTAEMSKFQOKNKGYCAQYRGVCNAVL-----AKDALVEL-NTSYADPEEAOELLVHT 354  
DB 301 ISTAEMSKFQOKNKGYCAQYRGVCNAVL-----AKDALVEL-NTSYADPEEAOELLVHT 354  
QY 355 ANNELKVPVPCRAEALCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKENLVME 414  
DB 355 ANNELKVPVPCRAEALCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKENLVME 414  
QY 415 EKHRLGLYSEMHLLSVPCSKSLPMSHMDPTACARLPHLDYKNEUKTEPPMTSSKPSVD 474  
DB 415 EKHRLGLYSEMHLLSVPCSKSLPMSHMDPTACARLPHLDYKNEUKTEPPMTSSKPSVD 474  
QY 478 IPRLP-ASTSSFAVSPAYSMYTIIVSSIALFALLTIYLYCCRRKKKKKRESTAV 536  
DB 478 IPRLP-ASTSSFAVSPAYSMYTIIVSSIALFALLTIYLYCCRRKKKKKRESTAV 536  
QY 535 TLTTPSELLEDRHPNPMYORPMLLPNKLLEYPNNIEYVRDISEGAFGRVQARA 594  
DB 535 TLTTPSELLEDRHPNPMYORPMLLPNKLLEYPNNIEYVRDISEGAFGRVQARA 594  
QY 597 PGLLPPEPTTMAVVKMLKEBASADQADFQREAAALMAEFDNPITVKLVGCAVGKRPCLL 654  
DB 597 PGLLPPEPTTMAVVKMLKEBASADQADFQREAAALMAEFDNPITVKLVGCAVGKRPCLL 654  
QY 655 FEYMAVGDLNEFLRSMSPHTVCSLSHSDLSMRQVSSPPGPPLSCAEOLCIAQOVAAGMA 714  
DB 655 FEYMAVGDLNEFLRSMSPHTVCSLSHSDLSMRQVSSPPGPPLSCAEOLCIAQOVAAGMA 714

DB 657 FEYMAVGDLNEFLRSMSPHTVCSLSHSDLSSTRARVSSPGPPPLSCAEOLCIAQOVAAGMA 716  
QY 715 YLSERKFVHRDLAPRNCVGENNVVKTADGCLSRNITYSADYKANKENDALPIRMPEST 774  
DB 717 YLSERKFVHRDLAPRNCVGENNVVKTADGCLSRNITYSADYKANKENDALPIRMPEST 776  
QY 775 FYNRRTESDVMAVGVLMWIFSGYLOPYGMAHEEYIVYVRDGNLISCPENCPELVYNL 834  
DB 777 FYNRRTESDVMAVGVLMWIFSGYLOPYGMAHEEYIVYVRDGNLISCPENCPELVYNL 836  
QY 835 MRLCWSKLPADRPSTSIHRIERMCERAGTVSV 869  
DB 837 MRLCWSKLPADRPSTSIHRIERMCERAGTVSV 871

RESULT 6

ID 061988 PRELIMINARY; PRT; 881 AA.

AC 061988; 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE NSK2 PROTEIN PRECURSOR.

GN MUSK OR NSK2.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=MYOBLAST;

RC MEDLINE=95349951; PubMed=7624144;

RA Ganju P., Walls E., Brennan J., Reith A.D.;

RT Cloning and developmental expression of Nsk2, a novel receptor

RT tyrosine kinase implicated in skeletal myogenesis,.";

CC Oncogene 11:281-290(1995). THE SER/THR FAMILY OF PROTEIN KINASES.

CC EMBL: X86445; CAA60166.1; -.

DR HSSP: P11362; IFGK.

DR MGD: MGI:103581; MusK.

DR InterPro: IPR002453; Beta.tubulin.

DR InterPro: IPR000719; Euk\_pkinase.

DR InterPro: IPR000024; Fz\_kinase.

DR InterPro: IPR003598; Fz\_c2.

DR InterPro: IPR003600; Ig\_c2.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR002290; Ser\_thr\_kinase.

DR InterPro: IPR001245; Ser\_thr\_kinase.

DR Pfam: PF01392; Fz; 1.

DR Pfam: PF00047; Ig; 3.

DR PRINTS: PR00109; TYRKINASE.

DR SMART: SM00408; IGC2; 2.

DR SMART: SM00410; IG-like; 1.

DR SMART: SM00219; Tyrc; 1.

DR PROSITE: PS50038; Fz; 1.

DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.

DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.

DR PROSITE: PS00228; TUBULIN\_B\_AUTOREG; 1.

DR ATP-binding; Immunoglobulin domain; Serine/threonine-protein kinase;

FT SIGNAL 1  
SQ SEQUENCE 881 AA; 98435 MW; EA0D028E9B28ED7 CRC64;

Query Match 90.3%; Score 4128; DB 11; Length 881;

Best Local Similarity 90.4%; Pred. No. 0;

Matches 788; Conservative 30; Mismatches 44; Indels 10; Gaps 4;

QY 1 MRELVINPVLHIITLVAFGSTETKLPKAPVITTPLETVDAIVEVATFMCVESTPOPEIS 60  
DB 1 MRELVINPVLHIITLVAFGSTETKLPKAPVITTPLETVDAIVEVATFMCVESTPOPEIS 60

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Db 1 MRELNIPLLOMLTLVAFSGTEKLPKPPVIATPLETVDAIVEEVAFTMCAYESYPOPEIS 60
QY 61 WTRKKILIKLEFDTYSIRENGQLTILSVESDDGIVCCTANNNGVGVESGALOYKMK 120
Db 61 WTRKKILIKLEFDTYSIRENGQLTILSVESDDGIVCCTANNNGVGVESGALOYKMK 120
QY 121 PKITRPPIVWKIEGLKAVLPCTTMGNPKPSVSIKSDPSIRENSRIAVLESGLRIHNV 180
Db 121 PKITRPPIVWKIEGLKAVLPCTTMGNPKPSVSIKSDPSIRENSRIAVLESGLRIHNV 180
QY 181 OKEDAGYRCVAKNSLTAAASKVYKLEFEVAFARILRAPESINVTFGSFVTLHCTATGPV 240
Db 181 OKEDAGYRCVAKNSLTAAASKVYKLEFEVAFARILRAPESINVTFGSFVTLHCTATGPV 240
QY 241 PTITWINGNAVSSGSIQESYKDRVIDSRLOLFTFKPGLYCIATNKHGEKFSAKAAAT 300
Db 241 PTITWINGNAVSSGSIQESYKDRVIDSRLOLFTFKPGLYCIATNKHGEKFSAKAAAT 300
QY 301 ISIAEMSKPOKDNKGCAOYRGVCNAVL-----AKDALVEL-NTSYADPEAOELLVHT 354
Db 301 ISIAEMSKPOKDNKGCAOYRGVCNAVL-----AKDALVEL-NTSYADPEAOELLVHT 354
QY 355 AMNELKAVSPVCRPAALALCNHFOECSPGVPTPIPGREYCLAVKELFCAEKELVME 414
Db 355 AMNELKAVSPVCRPAALALCNHFOECSPGVPTPIPGREYCLAVKELFCAEKELVME 414
QY 415 EKHARGLYRSEMLLSVPKCSKLPSEMDPTACARLPHLDYKNENLTFPPMTSSKPSVD 474
Db 415 EKHARGLYRSEMLLSVPKCSKLPSEMDPTACARLPHLDYKNENLTFPPMTSSKPSVD 474
QY 475 IPNIPSSSSSFSPYSPYIMTVIISMSRAIVLITTLTYCCRRKKOMKKRESAAV 534
Db 475 IPNIPSSSSSFSPYSPYIMTVIISMSRAIVLITTLTYCCRRKKOMKKRESAAV 534
QY 535 TLTLPSELDDLDRHPMPYORBPMLLPKLLSEYPRNNIEYVRDIEGEGAFGVPOARA 594
Db 535 TLTLPSELDDLDRHPMPYORBPMLLPKLLSEYPRNNIEYVRDIEGEGAFGVPOARA 594
QY 595 PGLLPYEPFTMAVAKMLKEBASADMDQAFORAEALMAEFDPNPVTKLLGVCAVSKPCLL 654
Db 595 PGLLPYEPFTMAVAKMLKEBASADMDQAFORAEALMAEFDPNPVTKLLGVCAVSKPCLL 654
QY 655 FEYMAVGDLEFLRSMSPHYVCSLSHSDLSMRAOVSSPGPPILSCAQLCTARVAAGMA 714
Db 655 FEYMAVGDLEFLRSMSPHYVCSLSHSDLSMRAOVSSPGPPILSCAQLCTARVAAGMA 714
QY 715 YLSERKEVHARDLATRNCLVGENNVYKJADEGLSRNYSADYKANKENDAIPIRMPPESI 774
Db 715 YLSERKEVHARDLATRNCLVGENNVYKJADEGLSRNYSADYKANKENDAIPIRMPPESI 774
QY 775 FYNRYTESOVWAYGVVLMIEFSTGLQPYYGMAHEEVIYVVDGNILSCPENCPVELYNL 834
Db 775 FYNRYTESOVWAYGVVLMIEFSTGLQPYYGMAHEEVIYVVDGNILSCPENCPVELYNL 834
QY 835 MRLCWSKLPADRPSPFHSIRLILERMCRARCT 866
Db 835 MRLCWSKLPADRPSPFHSIRLILERMCRARCT 866
QY 837 MRLCWSKLPADRPSPFHSIRLILERMCRARCT 868
Db 837 MRLCWSKLPADRPSPFHSIRLILERMCRARCT 868

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RP SEQUENCE FROM N.A.
RC TISSUE-ELECTRIC ORGAN, AND MUSCLE;
RC MEDLINE-93219391; PubMed-8385349;
RA Jennings C.G.B., Dyer S.M., Burden S.J.;
RT "Muscle-specific tyk-related receptor with a kringle domain defines a
RL distinct class of receptor tyrosine kinases.";
EMBL: L11311; AAA49285.1; -.
DR HSPB; P11362; IFGK.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: PF01392; Fz; 1.
DR Pfam: PF00047; Ig; 3.
DR Pfam: PF00051; kringle; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00018; KRINGLE.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00408; IGC2; 2.
DR SMART: SM00410; IG_Like; 1.
DR SMART: SM00130; KR; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS50038; Fz; 1.
DR PROSITE: PS00021; KRINGLE_1; FALSE_NEG.
DR PROSITE: PS50070; KRINGLE_2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; Immunoglobulin domain; Kinase; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 946 AA; 105892 MW; 81A9131DB7479D01 CRC64;

Query Match 63.4%; Score 2897; DB 13; Length 946;
Best Local Similarity 59.9%; Pred. No. 7.7e-252;
Matches 571; Conservative 113; Mismatches 169; Indels 100; Gaps 11;

QY 5 VNIPLVHILTLVAFSGTEK--LPKAVITPPLTVDAIVEEVAFTMCAYESYPOPEISWT 62
Db 6 VDIPLMLTF-LVTYGGSDGLILPKAPQITSPLETVDAIVEEASFCVAVDSYPAELTWT 64
QY 63 RNKILIKLEFDTYSIRENGQLTILSVESDDGIVCCTANNNGVGVESGALOYKMKPK 122
Db 65 RNPIPIRPEDRSTKENGQLTILSVEDDNGVYCTANNMGSSAOSGALOYKMKPK 124
QY 123 ITRPPIVWKIEGLKAVLPCTTMGNPKPSVSIKSDPSIRENSRIAVLESGLRIHNV 181
Db 125 IIRPPIVWKIEGLKAVLPCTTMGNPKPSVSIKSDPSIRENSRIAVLESGLRIHNV 184
QY 182 KEDAGYRCVAKNSLTAAASKVYKLEFEVAFARILRAPESINVTFGSFVTLHCTATGPV 241
Db 185 LEDAGYRCVAKNSLTAAASKVYKLEFEVAFARILRAPESINVTFGSFVTLHCTATGPV 244
QY 242 PTITWINGNAVSSGSIQESYKDRVIDSRLOLFTFKPGLYCIATNKHGEKFSAKAAAT 301
Db 245 TIKLENGRAVPAKSIQNRKIEGMEVSRARVYRSLFTCLTNKKNESSTAKATATL 304
QY 302 ISIAEMSKPOKDNKGCAOYRGVCNAVLADALVELNTSYADPEAOELLVHTAMNLEKV 361
Db 305 DIKEM-RLYKGDGLGCTSYGEGVCOGLLGOLVFFENSSPADDEGTOEMMARSTWELDG 363
QY 362 VSPVCRPAALALCNHFOECSP-GVYPTPIPGREYCLAVKELFCAEKELVMEKTHRG 420
Db 364 VSLCKPRAASLCLHFTFOCPNPLGLPTKLVCREHCLAVKELTKEMITMEDNSRIG 423
QY 421 LYSEEMLLSVKPSKLPSEMDPTACARLPHLD-----YKNENL----- 460
Db 424 VYSAG---LSLPDQGRLPSTIHPDEACTRVSLDMKKGIVTBMCYNNNGRFYQGSVAVTA 480

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QY 461 -----KTEPMTSS----- 469
DB 481 SGISCORSEBQAFHFRRLPEIPELANSDFCRNPGESERPMCYTMDIMREPCNP 540
QY 470 -----KPSVDIPNLPSSSSSFSFSPYTSMTVITISMSFAIFVLLITLTYCC 518
DB 541 QCINVSISSEMKRKTETAMPSTSA-----TYSMTVIISISLSLAASILLIITLTC 593
QY 519 RRRKMKNNK--RESAAVTLTLPSELLDRLPHPNPYOMPLLPKLSLEYPRNIE 576
DB 594 HHQKGLQTRSYTETETPLATLPSELLDRLPHPNPYOMPLLPKLSLEYPRNIE 653
QY 577 YVNDIEGAGRVFOARAPGLPEPTTVAVVKMLKEASADMQADFOREALMAEEDNP 636
DB 654 YVNDIEGAGRVFOARAPGLPEPTTVAVVKMLKEASADMQADFOREALMAEEDNP 713
QY 637 NIKKLGVCVAVGKPMCLLFYMAVGDNEFLRSMSPHTVCSLSHDSMAQVSSGPP 656
DB 714 NIKKLGVCVAVGKPMCLLFYMAVGDNEFLRSMSPHTVCSLSHDSMAQVSSGPP 773
QY 697 LSCAEOLCIAROYAAGMAYLSERKFVHRDLATRNCLVGENMYVKIADFGLSRNIYSADY 756
DB 774 LSCADQLNTAKQISAGMTYLSERKFVHRDLATRNCLVGEKLVYKIDFGLSRNIYSADY 833
QY 757 KANENDAIPIRMMPESIFNRTTSDVAVGVVLMETFSGLQPYGMAHEEVIYVR 816
DB 834 KANENDAIPIRMMPESIFNRTTSDVAVGVVLMETFSGLQPYGMAHEEVIYVR 893
QY 817 DGNILSCPEPCPELYNLMLRCLMSKLPADRPSTSIHRLIERMCEAEGTVSV 869
DB 894 DGNILSCPEPCPELYNLMLRCLMSKLPADRPSTSIHRLIERMCEAEGTVSV 946

RESULT 8
Q9DDA2 PRELIMINARY: PRT: 354 AA.
AC Q9DDA2:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MUSCLE SPECIFIC KINASE, TK DOMAIN (FRAGMENT).
GN MUSK.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RA Fu A.K., Smith F.D., Zhou H., Chu A.H., Tsai K.W., Peng B.H., Ip N.Y.;
RT "Xenopus MusK: Molecular cloning and prominent expression in neural
RT tissues."
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ222795; CAC19037.1;
DR HSSP: P1362; IFCG.
DR InterPro: IPR000719; Euk-kinase.
DR InterPro: IPR002290; Ser_thr-kinase.
DR InterPro: IPR001245; Tyr-kinase.
DR Pfam: PF00069; kinase.1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; STKC.1.
DR SMART: SM00219; TYRK.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
KW ATP-binding; Kinase; Transferase.
FT NON_TER 1
SQ SEQUENCE 354 AA; 40410 MW; 87BD2A217D95DDCE CRC64;

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QY 517 CRRRKMKNNKRESAAVTLTLPSELLDRLPHPNPYOMPLLPKLSLEYPRNIE 576
DB 2 CSRKQKTKMKNNKNEAAPITLALPSELLDRLPHPNPYOMPLLPKLSLEYPRNIE 61
QY 577 YVNDIEGAGRVFOARAPGLPEPTTVAVVKMLKEASADMQADFOREALMAEEDNP 636
DB 62 YVNDIEGAGRVFOARAPGLPEPTTVAVVKMLKEASADMQADFOREALMAEEDNP 121
QY 637 NIKKLGVCVAVGKPMCLLFYMAVGDNEFLRSMSPHTVCSLSHDSMAQVSSGPP 656
DB 122 NIKKLGVCVAVGKPMCLLFYMAVGDNEFLRSMSPHTVCSLSHDSMAQVSSGPP 181
QY 697 LSCAEOLCIAROYAAGMAYLSERKFVHRDLATRNCLVGENMYVKIADFGLSRNIYSADY 756
DB 182 LSCADQLNTAKQISAGMTYLSERKFVHRDLATRNCLVGENMYVKIADFGLSRNIYSADY 241
QY 757 KANENDAIPIRMMPESIFNRTTSDVAVGVVLMETFSGLQPYGMAHEEVIYVR 816
DB 242 KANENDAIPIRMMPESIFNRTTSDVAVGVVLMETFSGLQPYGMAHEEVIYVR 301
QY 817 DGNILSCPEPCPELYNLMLRCLMSKLPADRPSTSIHRLIERMCEAEGTVSV 869
DB 302 DGNILSCPEPCPELYNLMLRCLMSKLPADRPSTSIHRLIERMCEAEGTVSV 354

RESULT 9
Q9V6K3 PRELIMINARY: PRT: 724 AA.
AC Q9V6K3:
DT 01-MAY-2000 (G9TYH9; 096391;
DT 01-OCT-2000 (TREMBLrel. 13, Created)
DT 01-DEC-2001 (TREMBLrel. 15, Last sequence update)
DE BDNF/NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKB
DE TYROSINE KINASE) (NEUROSPECIFIC RECEPTOR TYROSINE KINASE) (NRK
DE PROTEIN) (CG4007 PROTEIN).
GN NRK OR KOR2 OR HD-434 OR CG4007.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Gelinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotlier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.P., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.J., Evangelista C.C., Ferraz C., Ferrier W.M., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Houston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaislin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pauley J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

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Query Match 35.1%; Score 1602; DB 13; Length 354;  
 Best Local Similarity 85.3%; Pred. No. 9,5e-136;  
 Matches 301; Conservative 21; Mismatches 31; Indels 0; Gaps 0;

RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svrtens R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissensbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveloff J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*,"  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Frith K.J., Scott M.J.;  
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 17-724 FROM N.A., AND CHARACTERIZATION.  
 RC TISSUE-IMAGINAL DISKS.  
 RX MEDLINE-97277331; PubMed-9115253;  
 RA Oishi I., Sugiyama S., Liu Z.-J., Yamamura H., Nishida Y., Minami Y.,  
 RT "A novel *Drosophila* receptor tyrosine kinase expressed specifically in  
 the nervous system. Unique structural features and implication in  
 developmental signaling,"  
 RT J. Biol. Chem. 272:11916-11923(1997).  
 RN [4]  
 RP SEQUENCE OF 586-638 FROM N.A.  
 RX MEDLINE-98401146; PubMed-9731193;  
 RA Oates A.C., Wolberg P., Achen M.G., Wilks A.F.;  
 RT "Sampling the Genomic Pool of Protein Tyrosine Kinase Genes using the  
 Polymerase Chain Reaction with Genomic DNA,"  
 RT Blochm. Biophys. Res. Commun. 249:660-667(1998).  
 RL [1]  
 CC -1- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),  
 CC NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR  
 CC (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE  
 CC NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN  
 CC SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-  
 CC GAMMA-1 (BY SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -> ADP + PROTEIN  
 CC TYROSINE PHOSPHATE.  
 CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW  
 CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURAL CELL LINEAGE FROM  
 CC EMBRYONIC STAGE 11 ONWARDS, RESULTING IN EXPRESSION IN THE BRAIN  
 CC AND VENTRAL NERVE CORD AT THE END OF EMBRYOGENESIS.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS IN EMBRYOS AND  
 CC LARVAE, LOW LEVELS IN ADULTS AND POBAE SHOW MAXIMAL EXPRESSION.  
 CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.  
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-  
 CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.  
 CC -1- SIMILARITY: THE REPEATED LEUCINE-RICH (LRR) SEGMENT IS FOUND IN  
 CC MANY PROTEINS. NUMBER IN THIS PROTEIN: 2.  
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC EMBL: AE003819; AAF58420.1; ALT\_INIT.  
 CC EMBL: AF0317164; AAD02091.1; -  
 CC EMBL: AB001420; BAA20134.1; -  
 CC EMBL: AJ002920; CAA05755.1; -  
 CC HSSP: P11362; IFG.  
 CC FlyBase: FBgn0020391; Nrk.  
 CC InterPro: IPR000719; Euk\_pkinase.  
 CC InterPro: IPR000024; Fz\_domain.  
 CC InterPro: IPR000001; Kringle.  
 CC InterPro: IPR001245; Tyr\_pkinase.  
 CC Pfam: PF00139; Fz\_1.  
 CC Pfam: PF00051; Kringle\_1.  
 CC Pfam: PF00069; pkinase\_1.  
 CC PRINTS: PR00018; KRINGLE.  
 CC PRINTS: PR00109; TYRKINASE.  
 CC SMART: SM00219; Tyrc\_1.  
 CC PROSITE: PS50038; Fz\_1.  
 CC PROSITE: PS00021; KRINGLE\_1; FALSE\_NEG.  
 CC PROSITE: PS50070; KRINGLE\_2; 1.  
 CC PROSITE: PS00107; PROTEIN\_KINASE\_ATP\_1.

DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 KW Transferrase: Tyrosine-protein kinase; Transmembrane; ATP-binding;  
 KW Phosphorylation: Receptor; Glycoprotein; Neurogenesis; Leucine-repeat;  
 KW Repeat: Immunoglobulin domain; Developmental protein; Signal.  
 FT SIGNAL 1 11  
 FT CHAIN 12 724  
 FT DOMAIN 12 322  
 FT TRANSMEM 323 343  
 FT DOMAIN 344 724  
 FT DOMAIN 48 83  
 FT REPEAT 48 61  
 FT REPEAT 62 83  
 FT DOMAIN 172 223  
 FT DOMAIN 243 279  
 FT DOMAIN 441 711  
 FT NP\_BIND 447 455  
 FT BINDING 475 475  
 FT ACT\_SITE 580 580  
 FT MOD\_RES 606 606  
 FT MOD\_RES 610 610  
 FT MOD\_RES 611 611  
 FT SITE 419 419  
 FT SITE 721 721  
 FT SITE 721 721  
 FT CONFLICT 51 51  
 FT CONFLICT 192 192  
 FT CONFLICT 306 306  
 FT CONFLICT 387 387  
 FT CONFLICT 391 391  
 FT CONFLICT 547 547  
 FT CONFLICT 706 724  
 SQ SEQUENCE 724 AA; 81836 MW; 0FFB9E1F7E4F6A26 CRC64;  
 Query Match 24.7%; Score 1129.5; DB 5; Length 724;  
 Best Local Similarity 38.0%; Pred. No. 1.2e-92;  
 Matches 263; Conservative 81; Mismatches 174; Indels 175; Gaps 21;  
 QY 310 QDNKGYCAQYRGECVNAVLAKDALVFLNLSYADPEEA--DELLVHTAMNEL-KVSPVC 366  
 DB 63 ERENGCYAPRSGKCKRYLYNGQWY----SLEPTGGMKNQYVTTALMDLISDGLC 118  
 QY 367 RPAEALLCNHIFDPC-SGVVPTPIPCREYCLAVKELFAKEDVMEETHGLYSE 425  
 DB 119 REAAEKMLCAVAFPCNHEGGRNAVAPLCFEDCAQTHLDFCYNDVWLIEEKERNMFLKS 178  
 QY 426 MHLISVPCSKLPMSHMDPTACARLPHDY-----N 456  
 DB 179 RGHFRLPNCSSLP-HYN-ASMRPNCSTYIGLEIKSEVSYDCRNGNGAFYMGTMNVS 234  
 QY 457 KENT-----KTF-PPWT-----SKRP-----SVDI 475  
 DB 235 KSGIRQWMDQYPRKHQPLVFEHQLLEGENCYCRNAGGERPHPCYTVDESVMQHDI 294  
 QY 476 P-----NLBSSSSSSBSVSPYTSMTVILISMSFAIFVL-LITTLTLCRR 521  
 DB 295 FMCPRDYVDPAVDLNTPIKMEKF---TPSMIFLAGIGFAVTLTLMITLVYKSKH 350  
 QY 522 KQWK-----NKKRE-----SAA 533  
 DB 351 KDYSOPAGAAVACSVSKRGCGGNGNINTSREILGNGNNTLAKMGTIRSTATIHNC 410  
 QY 534 VTLTLPSELLDLRLHPNMYORMPLNLPKILSLERYRNNEIYVRDIGEGAFVFGAR 593  
 DB 411 VALTTVTN--VSDAKGTR-----NARLEKLEYRGDIYVYRSIGGAFGVFGAR 459  
 QY 594 APGLIPEPTMVAVKMKLEASADMDQAFORBALMAEFPNPITVKLLGCAVKGKPMCL 653  
 DB 460 APGLVPDQEDDLVAVKMKLKDASDMQMDFEREACILAEFHPNIVRLIGYCALGRPMCL 519

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OY 654 LFEYMAVGDLNEFLRNSPHTVCSLSHSDLSMRAQVSSPGPPPLSCAEOLCIARQVAAGM 713
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 520 LFEYMAVPGDSEFLRACSPFATQAPQD---RLQLE-----LHLLQMANIATAGM 568
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 714 AYLSERKFFVARDLATRNCCLVGENMVKIADFGISRNITNSADYKANKANDAPIRMPPES 773
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 569 LYLSERKFFVARDLATRNCCLVGENMVKIADFGISRNITNSADYKANKANDAPIRMPPES 628
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 774 IFYRRTTESDVAAVGVLMVEIFSYGLOPYGMAHEVIYVVRDGNILSCPEKCPVELYN 833
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 629 ILNKTSLSDSWAVYICILMEVFSFALQPPFGLTHEEVITKTEGVNLGCPDNTPLSVIA 688
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 834 LMRCLWSKLPADRPSTST----HRLERMC 861
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 689 LMRCLWSKLPADRPSTST----HRLERMC 721
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
ID 09BK18 PRELIMINARY; PRT; 1145 AA.
AC 09BK18;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ROR.
OS Aplysia californica (California sea hare).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anasplidae;
OC Aplysiidae; Aplysia.
OX NCBI_TaxID=6500;
RN [1]
RP SEQUENCE FROM N.A.
RA McKay S.E., Hsiolop J., Scott D., Bulloch A.G., Kaczmarek L.K.,
RA Carew T.J., Sosasa W.S.;
RA "Aplysia for, a member of the Trk/Musk family of receptor tyrosine
RT kinases, forms clusters on the surface of identified neuroendocrine
RT cells.";
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC -1 CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL; AF216782; AAK25726.1; -.
DR HSRP; P11362; 1FGK.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR000024; Fz_domain.
DR InterPro: IPR003599; 1g.
DR InterPro: IPR003599; 1g.
DR InterPro: IPR003598; 1g_c2.
DR InterPro: IPR003600; 1g_like.
DR InterPro: IPR003606; 1g_MHC.
DR InterPro: IPR000001; Kintgle.
DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR002290; Ser_thr_Pkinase.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam; PF00047; 1g; 1.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR00109; TYRKINASE.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00410; IG_Like; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00031; Fz; 1.
DR PROSITE; PS00026; KRINGLE_1; UNKNOWN_1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
KW ATP-binding; Glycoprotein; Immunoglobulin domain; Phosphorylation;
KW Receptor; Transferase; Transmembrane.
SQ SEQUENCE 1145 AA; 125622 MW; 5C49FA6E2A9D1ABD CRC64;
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Query Match 21.2%; Score 966.5; DB 5; Length 1145;
Best Local Similarity 30.7%; Pred. No. 1,2e-77;
Matches 265; Conservative 99; Mismatches 278; Indels 221; Gaps 26;

OY 129 NVKIEELKAVLPCTMTGNPKPSVSWIK-----GDSPLRESRIAVLESGS 174
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 92 NVTKRGQAVRIGCEITGNPIPTISMTKDYIITNDSDRMKHKPTAMGR----- 143
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 175 LRIHNVQKEDAGQRCVAKNLSGTAYSKVYKLEFEVAFILRAPESHNTVFGSEFVLHCT 234
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 144 LKINDVRPSDSAVYTCKAENDFG-----NEETSGSLTVLNNEN 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 235 ATGIPYPTTIWINGNAVSSGSIQESYKDRVIDSRQLQFTFKRGLTCTATNKGKFFST 294
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 ---PPP-----SKSGGGSNNDDDDYPTPTDV-----VEGGEFFKKRYDT 215
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 295 AKAAATISIENWSPKQDNKGCAOYRGECVNCNVLAKDALVFLNTSVADPEEAOELLVHT 354
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 216 SVWPRDKDVEDDDKPR---DGFQITRGSTCAKFGVGMSTIYVTSKLTQSAEKKYMAFA 272
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 355 ANNELKVVSPVCRPAEALCNHIFQEGSPGV-VPTPIPCREYCLAVELFCAKEMLYM 413
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 273 VIGASSHMSQRCQOYGIQSLCYHAFPLCDKTADRPTRPKICRDECLAENDICRTLEYLM- 331
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 414 EERTHGLYRSEMHLLS---VPRCSKL--PSMHMDPTACARLPHLDYKKNELKTPPMTS 468
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 332 -AKRH-----NLIGDMLLPKCSQLQGPGR-BEDNCIIRI-----GMPPGST 370
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 469 S-----KPSYDIPNL-----PSSSSSEFSVPTSMYIISMSFAIVLLTTTLY 516
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 371 SGGRGKRGKGNPMNNNGTRDPRRGSGSGSKRPTDKDTGRQGP-----TDVY 421
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 517 CCRRRQ-----WKN-----KKRESAAVTLTT---LPS 541
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 422 CYTGRGTNYRGEVSVKSGFMCLGWKDSGFPELGDHNYCRNPNRGREDADWCFNDRKMK 481
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 542 ELL-----LDRLHPNP-----MYORMPL----- 560
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 482 ELCAVPRKCDYDEGHSSEADSESNKMTLITLSLTYPALGLILALICCSQSHNTRASR 541
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 561 -----LNPKLLS--LEYPRNNIEYVRDIGEGAFGRVQARAPGLPERPTM 605
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 542 PNKQAPVEMSLPNPKSSRAREFPMPIRLELGEAGFVKYGLGVLEGSSVTT 601
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 606 VAVKMLKEBASADMDQDFREAAIMAEFDPNPIVILGVCANQKPRCLLFEYMAQGDLE 665
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 602 VAKTLKENALKKQVNDREVDLMSDMRHPNIVCLGVCMKQEPVCMLEFYMAQGDLEH 661
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 666 FLRMSPHTVCSLSHSDLSMRAQVSSPGPPPLSCAEOLCIARQVAAGMALYSERKFVARD 725
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 662 YLLSHSPHSDDVTAABD-----SGTGGGHILEYSMLHVSQVAAGMETYLASHHFPVARD 715
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 726 LATRNCCLVGENMVKIADFGISRNITNSADYKANKANDAPIRMPPESIFVRYTTESDV 785
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 716 IAAKNILVADGLTVKISDFGLSRDYSDDYVSVQSKSLPVWMPPEALYKFTTDSYV 775
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 786 WAGVVLWEIFSYGLOPYGMAHEVIYVVRDGNILSCPEKCPVELYNLMRLCQWKLPRD 845
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 776 WAFGVLMVEIFSYGLOPYGFSNQEVIEMIRKQLLCPDECPANITGLMECHHMPAR 835
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 846 RPSFTSHRLERMCEAEGTVS 868
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 836 RPPFREIHTRLTW--RSELTTS 856
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
ID 09YH44 PRELIMINARY; PRT; 821 AA.
AC 09YH44;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
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DE NEUROTROPHIN RECEPTOR B XTRKB-ALPHA.  
GN XTRKB.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97101727; PubMed=8946245;  
RA Islam N., Gagnon F., Moss T.;  
RT "Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb  
RT mRNA are expressed in a pseudo-segmental manner within the early  
RT Xenopus central nervous system.";  
RL Int. J. Dev. Biol. 40:973-983(1996).  
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
CC TYROSINE PHOSPHATE.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC EMBL: U39670; AAD0001.1; -  
CC HSSP: P06213; IIRK.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003599; Ig.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR000483; LRR\_Cterm.  
DR InterPro: IPR000372; LRR\_Nterm.  
DR InterPro: IPR002011; Receptor\_tyr\_kin\_II.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00560; LRR; 1.  
DR Pfam: PF01463; LRCT; 1.  
DR Pfam: PF00069; Pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR SMART: SM00409; IG; 1.  
DR SMART: SM00082; LRCT; 1.  
DR SMART: SM00013; LRNT; 1.  
DR SMART: SM00219; TYRK; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
DR PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
DR ATP-binding: Glycoprotein; Phosphorylation; Receptor; Transferase;  
KW Transmembrane; Tyrosine-protein kinase.  
SQ SEQUENCE 821 AA; 92311 MW; 0AF81BE74FD8FED3 CRC64;

Query Match 17.6%; Score 802; DB 13; Length 821;  
Best Local Similarity 27.5%; Pred. No. 4.8e-63;  
Matches 239; Conservative 102; Mismatches 241; Indels 286; Gaps 24;

QY 24 LPKAPVITTPLEIVDALVEEATMCAVESTPPEISITRKILIKLFDTRYSTIRENQQL 83  
b 196 LPIANVSTV---NITVLEGNETTLYCDANGLPDPNVSWDIOIISK--KREMAKRPVL 249  
QY 84 LTIISVEDSD-GIYCCANGVGG---AVESGALQVKKMKPTTRPINKIIEGLKAV 139  
DB 250 LTLNANVSLDKRLITVCAENSVGDHISV---LNVHPPVITF--IDPLTDH-HWC 302  
QY 140 LPCTTGNPKPSVSMI-KGD-----SPLRENSRIAVLESGSLRIHNVQKEDAGQYR 189  
DB 303 IPFVGRNPKPTLQMFHNGNITSETDFIWSKIHETSNYTSNHHGLOLQDSPTHLNNGHYT 362  
QY 190 CVAANSIGTASKYVKLEFEVFAHILRPESHN-VTGESFTLHGTACIGIVPTTWLEN 248  
DB 363 LRAENITG-----RDRSRISALFPMKGPDPGNPTDPGEFYDETSDIG-GTSDTIGT 414  
QY 249 G--NAVSSGSIQSVKRVIDSRLQLFTRPGLYTCIAIKKHG--EKFSTAKAAATISI 303  
DB 415 GVTSTDSVNSNGNEDSITVYVVGIALVCT--GLVIMILLKFGHSHKSGKPSVSVS- 471  
QY 304 AEWSKPKQDNKGCAQYRGVEVCNAVLAQDALVFLNTSTADPEAOELLVHTAMNKLKAYS 363  
DB 472 -----NDSDSAS 478  
QY 364 PYCRPAEALLCNHIFQSCSPGVVPTPIPICREYCLAVKELFCAKEMVLMEKTRHGLYR 423

DB 479 PL-----HHI-----SNG----- 486  
QY 424 SEHHLSVPCSKSLPSMHPPTACARLPHDYKENIKTFPMTSSKPSVIDPNLSSSS 483  
DB 487 -----SNTSSSE 494  
QY 484 SFSVSPPTGSMFVILISMSFAIFVLLTITLYCCRRRQKMKKRESAAVLTITLPSL 543  
DB 495 GG-----PDYIGM----- 504  
QY 544 LLDRLHPNPKYQRPPLLNKRLSL-----EYRNNIEYVDIGEGAFGVQ 591  
DB 505 -----TKIPYIENPOYFGITNSHUKSDTFVGHIRHNINVLKRELGEAGFVFL 553  
QY 592 ARAAGLLPYEPFVWAVKMKKEESADMOADFOREALMAEPDNPINVLKLGVCANQKPM 651  
DB 554 AECYNLYPEQDKILVAVKTLK-DASDNARQDFHREALNLNLOHEHIVKRYGCVESDPL 612  
QY 652 CLTFEYVAYDNLNEFLKSMSPHTVCSLSHSDLSMRAQVSSPPPLSCAQLCTIAROVAA 711  
DB 613 IMVEYMKHGDINKFLRAHGPDAV-----LMAEGNRPAELTQSOMLHTAQOIAA 661  
QY 712 GMATLSERKRYHRLATRNCLVGENMYKTADEGLSRNYSADYYKANENDAPIRMP 771  
DB 662 GMVYLASQHFVHRDLATRNCLVGENLLVKIGDFQMSKDVSTDYRVGGHTMLPIRMMP 721  
QY 772 ESIFYNRYTDESQVWYAVYLMELFSGYLOPYGMAHEEYIYVVRDGNILSCPNCEVEL 831  
DB 722 ESIMYKRFTESDVWMSLGVYLMELFTYQKOPWYLSNNEVECTIGQRVLRPTCRKEV 781  
QY 832 YNMLRLCWSKLPADRPSEFTHIRLERM 859  
DB 782 YDLMIGCMQREPHRMRLNIKEIHSLLQNL 809

RESULT 12  
ID Y43 PRELIMINARY; PRT; 811 AA.  
AC Q9YH43;  
DT 01-MAY-1999 (Tremblrel. 10, Created)  
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE NEUROTROPHIN RECEPTOR B XTRKB-ALPHA.  
GN XTRKB.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97101727; PubMed=8946245;  
RA Islam N., Gagnon F., Moss T.;  
RT "Catalytic and non-catalytic forms of the neurotrophin receptor xtrkb  
RT mRNA are expressed in a pseudo-segmental manner within the early  
RT Xenopus central nervous system.";  
RL Int. J. Dev. Biol. 40:973-983(1996).  
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN  
CC TYROSINE PHOSPHATE.  
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).  
CC EMBL: U39671; AAD0002.1; -  
CC HSSP: P06213; IIRK.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR003599; Ig.  
DR InterPro: IPR001611; LRR.  
DR InterPro: IPR000483; LRR\_Cterm.  
DR InterPro: IPR000372; LRR\_Nterm.  
DR InterPro: IPR002011; Receptor\_tyr\_kin\_II.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00560; LRR; 1.  
DR Pfam: PF01463; LRCT; 1.  
DR Pfam: PF00069; Pkinase; 1.





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QY 44 VATEPCAVESYPOPEISWTRKILKLEDPTRYISRENGQLTILSVED----- 91
DB 139 LTT-----LSW-----QLFOT--LSLRE-----LQLEQNFENCSCDIRM 171
QY 92 -----SDGIIYCCCTANNVGA-----VSCGALOVKMKPKITRPINVKI 132
DB 172 QLMWBOGAKLNSQNLVYICIND-----GSQPLFRNNISQCDL-----PEISVSHVNLTV 221
QY 133 IEGTLAVLPCTTGMKPKSVSMI-----KGDSPLENSRLAVESGSLRIHVOKEDAG-Q 187
DB 222 REGDNAVITTCNGSGSPLEDDVIMVITGLSINTHOTNLMTWVHAINLVLVNTSEDNGFT 281
QY 188 YRCVAKNSIG-----TAY--SKVVLLEFEVFAILRADE---SHNVTEGSEVTLTCT 234
DB 282 LTCIAENVVGNMSNVALTYVPPRVSL-----EPRLRHEHIEF-----V 324
QY 235 ATGIVPPTITMENGNVSSGI--QESVQDRVIDSLQLTITKP-----GLYCIATNK 287
DB 325 VRGNPPTLHMLHNGOPLRESKILHVEYVQGEISEGCLP--NKPTHYNNGNVTLIAKNP 383
Y 288 HGEKSTAKAATISIAEMSKPQKDKNGCYAOYRGEVGNVLAQALVFLNTSVADPEEA 347
DB 384 LG-----TAQOTIN-----GH-----FLKEPF--PEST 404
QY 348 QELLVHTAMNELKVSPVCRPAEALLCNHIFOECSPGVPTPIPICREYCLAVKELECA 407
DB 405 DNEI-----LEDEVSP----- 415
QY 408 KEMLVMEKTRGLRSEMHLLSVPKCKSLPSMHMDPTACARLPHLDYKNENKLTTPPMT 467
DB 416 -----TPBIT 420
QY 468 -SSRPVDIPNLPSSSSSFSVPTYSMTVTIISMSFAIVLLTTLTYCCRRRKKMN 526
DB 421 VTHKPEED-----TFGVSIIVGLAARFCVLLVLFVWINKYGRSKNGM 464
QY 527 K-----KRESAAVTL-----TLPSELILLDLRHPNM---YORMLPLNPKILLSLEY 570
DB 465 KGPVAVISGEDSDASPLHINHNGITTPSSL--DAGPDTVIVIGMTRPIVENPQYFRQGH 521
QY 571 -----PRNNIEYVDIGEGANGRYFOARAROLLYEPFTMYAVAVMLKEASAD 618
DB 522 NCHRPDTYVOHIIKRRDYLKRELEBAGKVFLECYNLSTPKDKMLVAVALDPTLA- 580
QY 619 MOADFOREALAMAEFDNPNYIKLLGVCAVGRKMLLEFYAAGGDLNEFLRSMSPHTCSL 678
DB 581 ARKDFORARELLTNIQHHIYKFGVCGDGPRLIMVEYMKHGDNLKFLRAHGD----- 635
Y 679 SHSLSMRAQVSSPGPP-----PLSCABQLCIAQOVAAGMAYLSERKFVHRDLATRNCLV 733
DB 636 -----AMLIVGQPRQAKGELGSLQMLIASQIASGMVYLASQHFVHRDLATRNCLV 687
QY 734 GENNVYKIADEGLSRNYSADYK--ANEND-----AIPIRMPPESEIFNRY 779
DB 688 GANLVKIKGDFGMSRDYSTDYKLPNPSGWDCEICWEGVGHMLPIRMPPESEIMRK 747
QY 780 TTESDVAVGVVLEIFSYGLQPYGMAHEVLYYVRDGNILSCPEKCPVELYMLMLCW 839
DB 748 TTESDVMSFGVILWEITFYGQPFQLSNTEVICITQGRVLERPRVCKREYIVVMLGCW 807
QY 840 SKLPADRPSTSIHRIER 859
DB 808 QREPOQRLNIKEIKLIAL 827

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RESULT 14
Q24488 PRELIMINARY; PRT; 685 AA.
AC Q24488;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

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DE TYROSINE-PROTEIN KINASE TRANSMEMBRANE RECEPTOR ROR PRECURSOR
DE (EC 2.7.1.112).
GN ROR OR CG4926.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=CANTON-S; TISSUE=LARVAL BRAIN;
RX MEDLINE=9348222; PubMed=8394009;
RA Wilson C., Guberhan D.C.I., Steller H.;
RT "Drosophila: a potential neurotrophic receptor gene, encodes a Drosophila
RT homolog of the vertebrate Ror family of Trk-related receptor tyrosine
RT kinases.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis J.R., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.E., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandal D., Bolashkov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier A., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garcia N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
RA Jasthi M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,
RA Palazolo M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Stryker R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE OF 545-597 FROM N.A.
RX MEDLINE=98401146; PubMed=9731193;
RA Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
RT "Sampling the genomic pool of protein tyrosine kinase genes using the
RT polymerase chain reaction with genomic DNA.";
RL Biochem. Biophys. Res. Commun. 249:660-667(1998).
CC -1- FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR THAT FUNCTIONS DURING
CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
CC TYROSINE PHOSPHATE.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN NEURONS OF THE DEVELOPING NERVOUS
CC SYSTEM.

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DR PROSITE; PS50038; FZ; 1.  
 DR PROSITE; PS50070; KRINGLE\_2; 1.  
 DR PROSITE; PS50107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS50109; PROTEIN\_KINASE\_TYR; 1.  
 KW ATP-binding; Immunoglobulin domain; Kinase; transferase.  
 SQ SEQUENCE 928 AA; 103864 MW; F13B8C9BCAB30D20 CRC64;

Query Match 16.9%; Score 773.5; DB: 5; Length 928;  
 Best Local Similarity 24.7%; Pred. No. 2.2e-60; Mismatches 309; Indels 275; Gaps 32;  
 Matches 237; Conservative 139;

QY 87 LSVEDSDGICCTANGVGAVGSCALGVKMP--KTRPPINVKIIEGLKAVLPCTT 144  
 DB 10 LVLEPADD-----BGLHGNASMEGTSGORPYIRLTQLNRNATKSSGDEVRKCEA 61  
 QY 145 MGNRPVSVWIKGDSPLRENSRIAVL---SGSLRIHNVKEDAGQRCVAKNSLGTAYS 201  
 DB 62 LGTPPLKFIWKNNGPVEKTRKVKIRDKENSSRLVITQLDVLDSGYQCIVSNPAASVNT 121  
 QY 202 KVKLEFEVFRILRAPE-----SH---NVTFGSEVTLHCTATGIPPTIWIEN 248  
 DB 122 TSV-----LRVNNVPAAVLSOKGSHSTKHAFDEY-----ED 156  
 QY 249 GNAVSSGSI---QESVKDRVIDSRQLFTIRGLYTCTIATNKHGEKFTAKAANTISAE 305  
 DB 157 YEMDRGRLLPDEEDADLRVPD-----AAGSNYAPVAVSE 192  
 QY 306 -WSRPQKNKGYCAQYRGECVNAVLAQDAVFLNTSYADPEE---AOELLVHTANNE 358  
 DB 193 RMLDGIRKRVGDCVQYRGACROYLSNKFVAMTNSREMYDIDRNLRAMLFI---NG 248  
 QY 359 LKVVSPVCPAPAEALLCNHIFQECSPGVVPPPIPICREYCLAVKELFCAKEWLVME--- 415  
 DB 249 APTISQKCRQLSQAVACHHMYKVCESDSNNQIVSICKHDCVITQNDCEPSELALAAQHEL 308  
 QY 416 --KTRGLYRSMHLISVPKCKSLPS-----MHW----- 442  
 DB 309 VGDTPKALF-----PLCSRLLSTSNCTIYVMTALOSSPYAEVNRGHLTHWCYVNSG 359  
 QY 443 -----DPTACARLPHLDYNKE--NLKTFP-----PMTSKP 471  
 DB 360 TQYEGVNAQTSSGKQCA--PWIDSTSRDENVHRFELMNSKNYCRNPGKKSPWCYSKP 417  
 QY 472 S-----VDIPNLPSS-----SSSSFSVSPYSMTVLIISIMS---FA 505  
 DB 418 MGOEYCDVPQCPDMDYPHLNDKVEGSKGCVSESYTALMDSLDPTMQVALVGGGVFS 477  
 QY 506 IFVLITITTLGCCRRRKQKNNKRESAAVLTLPSEL-----LLDR 547  
 DB 478 LLLLLFCACCCCRRAK--KSKQTRHQNAHCSAPSVINSANASAYYRKINGTSTPIMGR 535  
 QY 548 LHPN-----PMYQRMPLLLNPKLLSLEYPRNNIEY-----VRD- 580  
 DB 536 VPHVEMTSLIPSAQHLGPPYPMQHLQOARFPPOEPLIDNSYKVFETTPQSLSVREK 595  
 QY 581 IGGAGRGVYFOA--RAPGLLPYEPFTWAVAKLKEASADMQADFQREALMAEFDPNIV 639  
 DB 596 IGGGQGVVHSGIYTSGLFAPRPM--VAVKCKCHDATNAERAOLEDQIRAVATEFDHPNVI 654  
 QY 640 KILGCAVGRPKCLFEYMAVGDINEFLRSMSP---HTVCSLSHSDLSMRAQVSSPGRP 696  
 DB 655 KLIGVCMYMDNSLAVFEYVHGDHLELKVVPADHDGITEAN----- 700  
 QY 697 LSCAEQCLARQVAAAGAAVYSEKRFVHRDLATRNCLIGENNVYKIADEGLSRNYSADY 756  
 DB 701 ---AEFLYIAQIALGMEYTLASMSFVRDLATRNCLVGDTRTIKINADFGLMRTSYGSDY 757  
 QY 757 KANENDAIPIRMPPESIFNRYTTESDVAVYGVVLEIFSYGLQPYGMAHEVYIYVR 816  
 DB 758 KMLHRSMYPRWMSKEAIEDGRFSEASDVMSFVTLMEIWSFGROPYEGASMQVIELVA 817

QY 817 DGNILSCPEPCPELYNLMLRCLWSKILPADRPSFTSI-----HRIERMOCERA 863  
 DB 818 NRHLLECPHNCPTNITYSLMVECWHEHNTERRPTSEIRSRLOWSLASPAHSILQGHNNRA 877

Search completed: August 16, 2002, 13:38:33  
 Job time: 153 sec





CC method uses a mutated PKR nucleic acid which comprises a modification  
 CC to the intracellular and extracellular domains, or comprises a  
 CC modification to the intracellular domain and excludes any nerve growth  
 CC factor receptor(s) (NGFR). The method uses mutated PKR as a cell  
 CC surface marker, and is useful for identifying genetically modified cells,  
 CC especially immunoselection of transduced mammalian cells, and for  
 CC identifying mammalian cells expressing a protein of interest. The  
 CC genetically modified cells may be used in an autologous or  
 CC allogeneic setting e.g. gene therapy for bone marrow transplants, graft  
 CC facilitation or immune reconstitution.

XX Sequence 869 AA:

Query Match 100.0%; Score 4569; DB 22; Length 869;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 869; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRELVIPLVHITLVAISGTEKLPKAPVITTPLETVDAIVEVATFMCVAVESYPOPEIS 60  
 DB 1 mrelvnpivhlitlvaifagtekikpavlttpletvdaivevatfmcavesyppeis 60  
 OY 61 WFNKLIKLFDRYSIRENGQLLTLSVSDSDGTYCCANNVGAVESGALQVKKM 120  
 DB 61 wfnklliklfdrcysirengqltllsvdsddgtyccannvgavescgalqvkkm 120  
 OY 121 PKITRPINWKITEGKAVLPCTTMGNPKPSVSMIKGDSPLRENSRIAVLESGSLRIHNV 180  
 DB 121 pkitrpinwkitegkavlpcttmgnpkpsvsmikgdsplrensrilavlesgslrihmv 180  
 OY 121 PKITRPINWKITEGKAVLPCTTMGNPKPSVSMIKGDSPLRENSRIAVLESGSLRIHNV 180  
 DB 121 pkitrpinwkitegkavlpcttmgnpkpsvsmikgdsplrensrilavlesgslrihmv 180  
 OY 181 OKEDAGQYRCVANKSLGTAVSKVYKLEFEVFAIRILRAPESHNTFGSFVTLHCTATGIPV 240  
 DB 181 okedagqyrcvankslgtavskvyklefevfarilrapeshntfgsfvltlhcatacipv 240  
 OY 241 PTTTWENGNNAVSSGSIQSVKRVIDSRLQLEFTRKGLYTCTATNKHGKESTAKAAAT 300  
 DB 241 ptttwengnavssgsiqsvkrdvdsrlqlftrkgltyctatnkhgkfstakaaat 300  
 OY 301 ISTAENSKFOKDNKGCAQYRGEVCNAVLAKDALVFLNLSYADPEEAOELLVTTANNELEK 360  
 DB 301 istaenskfokdngcayrgevcnavlakdalvflnlsyadpeeaelvltanmek 360  
 OY 361 VVSPVCRPAEALLCNHIFQECSPGVVPPPIPCREYCLAVKELFCAKELVMEKTHRG 420  
 DB 361 vvspvcrpaeeallcnhifqecspgvvppiprcreyclavkelcfakewlmeekthrg 420  
 OY 421 LVRSSEHLLSVKCSKLRPMHMDPTACARLPHIDYKMKNTKPPMTSSKPSVDINDLPS 480  
 DB 421 lvrssehlhsvkcsklrpmhmdptacarlphidynkenlktprmtsskpsvdiplps 480  
 OY 481 SSSSSFSVSPYSMTVLIISIMSSFAIFVLTITTLVCCRKRKQMKKKRBSAAVTLTTLR 540  
 DB 481 sssssfsvspysmtvliisimssfaifvltitlvcrrkrkqmkkkrsaaavltiltr 540  
 OY 541 SELLDRLRPNRYQMPPLLNPKLISLEYPRNNITEYRDIGGAGRGVQARAGLLPY 600  
 DB 541 sellldrlrpnryqmppllnpkllisleypnniteyrdigagrgvqaragllpy 600  
 OY 601 EFFTAVAVMLKEEASADQADQADREAAALMAEFDNPNTIKLLGCVAVGKPMCLFEYMAV 660  
 DB 601 eeftavavmlkeeadadqadqreaaalmaefdnpnitkllgvcavgkpmcllfeymav 660  
 OY 661 GDLINEFLRSMSPHTVCSLSHSDLSMRAQVSSPPPLSCAEQICIAQVAAAGAAVSEK 720  
 DB 661 gdlineflrsmshphtvcsllshdsdlsmaaqvssppplscaeqiclarvaaagaaavsek 720  
 OY 721 FVHRDLATNCLVGENMVKIADFGLSKNITYSADVYKANENDAIPIRRMPPEISFYNNRYT 780  
 DB 721 fvhrdlatnclvgenmvkiadfglskniysadvykanendaiplrmppeesifynryt 780  
 OY 781 TSSDVAAVGVLMELFISYGLQPYGMAHEEVITYYVVDGNIILSCPEKCPVELNMLTCLMS 840  
 DB 781 tssdvavgvvlmelfisylqpygmaheevityyvvdgnilscpencpelynmltclms 840

OY 841 KLPADRPFSIRHILERMCEAGETVSV 869  
 DB 841 klpadrpfsirhilermerceregvtsv 869

RESULT 3  
 AAW26611  
 ID AAW26611 standard; protein; 869 AA.  
 AC AAW26611;  
 AC AAW26611;  
 DT 27-JAN-1998 (first entry)  
 XX Human muscle-specific kinase (MUSK).  
 DE Receptor tyrosine kinase; muscle specific kinase; MUSK; Dmk; human.  
 KW ligand; agrin; diagnosis; therapy.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 OS MO9721811-A2.  
 PN 19-JUN-1997.  
 PD 13-DEC-1996; 96WO-US20696.  
 PF 10-MAY-1996; 96US-0644271.  
 PR 15-DEC-1995; 95US-0008657.  
 XX (REGG-) REGENERON PHARM INC.  
 PA Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD;  
 PI WPI, 1997-332783/30.  
 DR N-PSDB; AAT90473.  
 XX

PT Nucleotide sequences encoding human agrin and muscle specific kinase  
 PT and related receptor - used in diagnosis and treatment of disorder  
 PT with muscle atrophy  
 XX

PS Example 4; Fig 4; 120pp; English.  
 XX

XX This polypeptide comprise a novel human receptor tyrosine kinase  
 CC designated and denervated muscle. Musk is alternatively referred to  
 CC Dmk for denervated muscle kinase. The amino acid sequence was  
 CC deduced from an isolated cDNA clone (see AAT90471). Rat Musk (see  
 CC AAW26610) has also been identified. Use of Musk to generate anti-  
 CC Musk antibodies and in the diagnosis of neurological or other  
 CC disorders is disclosed. Assay systems that may be used to detect  
 CC and/or measure ligands that bind the musk gene product are provided.  
 CC A claimed method of promoting the growth, differentiation or  
 CC survival of Musk receptor-expressing cells involves administration  
 CC to the cell of agrin (see AAW26609). Such cells include muscle,  
 CC heart, spleen, ovary and retina cells, or cells genetically  
 CC engineered to express the Musk receptor.  
 XX

XX Sequence 869 AA:

Query Match 99.8%; Score 4558; DB 18; Length 869;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 MRELVIPLVHITLVAISGTEKLPKAPVITTPLETVDAIVEVATFMCVAVESYPOPEIS 60  
 DB 1 mrelvnpivhlitlvaifagtekikpavlttpletvdaivevatfmcavesyppeis 60  
 OY 61 WFNKLIKLFDRYSIRENGQLLTLSVSDSDGTYCCANNVGAVESGALQVKKM 120  
 DB 61 wfnklliklfdrcysirengqltllsvdsddgtyccannvgavescgalqvkkm 120



Oy	121	PKIIRPPINNAKIIIEGKAVLPCTTMGNPKRSVSMIKDSPLREKSRNAVLESSLRHNH	180
Db	121	pkltprptnvnklliegkavlpcttmgnpkrsvswikdpslrenstrlavlesgslthnv	180
Oy	181	QKEDAGQRCVAKNSLSGTAYSKVYKLFEEFVARILRAPESHNVPFGSFVLHCTARGIPV	240
Db	181	qkedagqrcvaknsldgtayskvklfevfarilrapeshnvtfgsvflhctargipv	240
Oy	241	PTTIWIENGNAVSSGSIQESYKDVIRDSRLQLEPTFKGLYTCTATNKHGEKSTAKAAAT	300
Db	241	pttiwiengnavssgsiqesvkdvdvirdslqlflltkpgllytclatnhgskfstakaaat	300
Oy	301	ISIEWMSPOKDNKGCYAOYGEVCNNAVLKADALVFINTSYADPESEKQELVTANNELK	360
Db	301	isiewskpdkdnkgycaqyrgvccnavlakdavlfnintyadpeeeagellvhtawelk	360
Oy	361	VSPVPCRPABALLCNHIFQECSPGVVPTPIPICREXCIAVKELFCAKEWLVNEERTHRG	420
Db	361	vspvpcrpaeeallcnhifqecspgvvptpripicrexciavkelfcakewlvneekthrg	420
Oy	421	LYRSMHLLSVPKCSKLPMSMHMDPTACARLPHLDYKNENKTPRPMSSKPSVDIPLPS	480
Db	421	lyrsmhllsvpckslpmsmhmdptacarlphldykenkkltpmsskpsvdiplpss	480
Oy	481	SSSSFSFVSPYSMTVIISIMSSPAIEVLLITTLTYCCRRRKQMKKKKRESAAVTLITLP	540
Db	481	sssfsvspysmtvtvliissmstfaivllitltlyccrrrkqmkkkkresaaavtlitlp	540
Oy	541	SELLIDRLRHPNMQORPBLNLPKLLSLEVEPRNNIEVVRDIOGCAFGCRVQAARPGILPY	600
Db	541	sellidrlrhpnmqorpmllnprkllsleypnmilevridgeaigrvfqtargpdlpy	600
Oy	601	EPTFWAVAKMLEEASADMDQADFQREAAALAEFNPNTIVKLLGCAVGRKPMCLLFEXMAY	660
Db	601	epftmwavakmleeeasadmdqdfqreaalaeefnnpntivkllgvcaqgkpmcllfeymay	660
Oy	661	GDLENFLRSMSPRHVVCISHSDSLMSRAQVSSPPCPPLSCAEQICIAOVAAGMAYISERK	720
Db	661	gdlneflrsmsprhvcslshsdlsmsraqvssppcpplscaeqiclaqvaaagmayiserk	720
Oy	721	FVHRDLATRNCLVGENNVYKTADEGLSRNTIYSADYIKANENDAIPIRMPPESTIFYNRYT	780
Db	721	fvhrdlatrncldvgenmvvkaadqglslrnlylsadyikanendaipirmppestifynryt	780
Oy	781	TESDVWAVGVVLMELFSTGLQPIYGVMAHEEVIYVRDGNILSCPENCPVELYNLMRLCWS	840
Db	781	tesdvwavgvvvllmelfstgldpiygvmaheeivyvrldgnilscpencpvelynlmrlcws	840
Oy	841	KLPADRPSTSIHRLTERMCRACGATVSV	869
Db	841	klpadrpstsihrltermceracgattsv	869
RESULT 4			
ID	AAW26506		
XX	AAW26506	standard; Protein: 869 AA.	
XX	AAW26506:		
XX	06-JAN-1998	(first entry)	
XX	DE	Human Dmk receptor.	
KW	Dmk receptor: tyrosine kinase receptor: signal transduction; assay;		
KW	therapy; diagnosis; Alzheimer's disease; Parkinson's disease;		
KW	amyotrophic lateral sclerosis; Lou Gehrig's disease;		
KW	idiopathic torsion dystonia; muscle atrophy.		
OS	Homo sapiens.		
XX	PN	US5656473-A.	
XX	PD	12-AUG-1997	

Accession	Sequence	Score	DB	Length	Query Match
XX	21-JUL-1993; 93US-0095658.	99.8%;	DB 18;	Length 869;	Query Match
XX	19-JAN-1995; 95US-0374834.	99.8%;	Pred. No. 0;		Best Local Similarity
XX	21-JUL-1993; 93US-0095658.	1;	Mismatches 1;	Indels 0;	Gaps 0;
XX	(REGE-) REGENRON PHARM INC.				
XX	Rojas EA, Valenzuela DM;				
XX	WPI, 1997-414593/38.				
XX	N-PSDB; AAT87073.				
XX	New isolated human denervated muscle kinase receptor - used to develop products for the diagnosis and treatment of neurological, muscle or neuromuscular disorders				
XX	Claim 4; Column 31-36; 31pp; English.				
XX	This polypeptide comprises the human Dmk receptor (AAW26506), a novel tyrosine kinase receptor that is expressed in high levels in denervated muscle. Its amino acid sequence was deduced from an isolated nucleic acid molecule (see AAT87073). The Dmk receptor can be used to screen for agents that interact with Dmk. Agents that bind to the receptor may mediate survival and differentiation in cells naturally expressing the receptor, but may also confer survival and proliferation when used to treat cells engineered to express the receptor. Dmk receptor polypeptides and polynucleotides can also be used for detecting aberrancies in the function or expression of the receptor which may be used in the diagnosis of muscular or other disorders. Manipulation of the receptor or agonists which bind this receptor may be used to treat neurological diseases, diseases of muscle or neuromuscular unit disorders, including Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis (Lou Gehrig's disease), idiopathic torsion dystonia and muscle atrophy. The extracellular domain (ECD) of the receptor can be used to block the binding of receptor to target cells. A receptorbody comprising the ECD fused to a human Ig gamma-1 constant region is claimed.				
XX	Sequence 869 AA:				
XX	1 MEEVNIPIVLITLIVAFSGTEKLPKAPVITTPLETVDAIVEAVTFKAVESYPOPEIS 60				
XX	1 melvniplvhlitlivaafsgteklpapyitlptletvdalveavtfmcavesyppeis 60				
XX	61 WTRNKLILFPTPRTSIRENGSGLTLTISVEDSDGICTANNNGGAAVSGALGVKK 120				
XX	61 wrnkllilfdtrysirngqlltlisvedsdgilyctannnggaaavgaaagcalgvkkn 120				
XX	121 PRTIRPPIVWKLIEGKAVLPCTMTGNPKPSVSWIKGSDPLRENSRIAVLESGLRIHW 180				
XX	121 prtirppilvwliegkavlpcctmtgnpkpsvswikgdsplrensriavlesgsrlrhnv 180				
XX	181 QKEDAGQYICVAKNSIGTAYSKVYKLEFVFPARILRAPSHNVTCSTFTILCTATGIPV 240				
XX	181 qkedagqycvacknsigtayskvvyklevfarilrapshnvitcstftilctatgipv 240				
XX	241 PTTWTENENNAVSSGSIQSVKDRVIDSLQFTFPGYTCIATNKHGEKSTAKAAAT 300				
XX	241 pttwtengenavssgsiqsvkdryidslrlqftfpglytciatnkhgekstakaat 300				
XX	301 ISIAEWSKQKONKGYCAQYRGECNAVLAKDALVFLNTSYADPEEAOELLVHTAMNKL 360				
XX	301 isiaewskpqkdnkgycagyrgecnavlakdalvflntsyadpeeagllvhtamnelk 360				
XX	361 VVSPVCRPAABALCNHIFQECSPGVPRPIPIGRYCLAVNELCAKRWLMEEKTHG 420				
XX	361 vvspvcrpaagalcnhifqecspgvprpdpicreyclavnelcaakwlmeeekthg 420				

QY 421 LKSEHMLLSVPCSKLPSNHHMDPTACARLPHLDYKNENLTPPPMTSSKPSVDINPLPS 480  
DB 421 LKSEHMLLSVPCSKLPSNHHMDPTACARLPHLDYKNENLTPPPMTSSKPSVDINPLPS 480  
QY 481 SSSSSFSVSPYSMTVIISIMSSFAIFVLLTTITLTCRRRKQWKKKRSAAVTLTTLTLP 540  
DB 481 SSSSSFSVSPYSMTVIISIMSSFAIFVLLTTITLTCRRRKQWKKKRSAAVTLTTLTLP 540  
QY 541 SELLDRLHPNPMYQRMPLLNPKLLSLLEYPRNIEVVDIGGAGRGVQOARAPGLLPY 600  
DB 541 SELLDRLHPNPMYQRMPLLNPKLLSLLEYPRNIEVVDIGGAGRGVQOARAPGLLPY 600  
QY 601 EPTTMAVAVKMLKEASADQADFOREALMAEFDNPNIYKLLGVCAVGKPMCLLFEXMAY 660  
DB 601 EPTTMAVAVKMLKEASADQADFOREALMAEFDNPNIYKLLGVCAVGKPMCLLFEXMAY 660  
QY 661 GDNIEPLRSMSPHYVCSLSISDLSMRQVSSPPPLSCAEQICIAQVAAAGMAYLSEBK 720  
DB 661 GDNIEPLRSMSPHYVCSLSISDLSMRQVSSPPPLSCAEQICIAQVAAAGMAYLSEBK 720  
QY 721 FVHRDLATRNCLYGENNVKVIADFGLSRNITYSADYYKANENDAIPIKMPPESTFYNYRT 780  
DB 721 FVHRDLATRNCLYGENNVKVIADFGLSRNITYSADYYKANENDAIPIKMPPESTFYNYRT 780  
QY 781 TESDWAYGVVLMWIFSYGLQPYGYMAHEEVITYVRDGNILSCPENCPELVNLMRLCWS 840  
DB 781 TESDWAYGVVLMWIFSYGLQPYGYMAHEEVITYVRDGNILSCPENCPELVNLMRLCWS 840  
QY 841 KLPADRPSTSIHRIELERMCEBAGTYSV 869  
DB 841 KLPADRPSTSIHRIELERMCEBAGTYSV 869

RESULT 5  
AAW26610  
ID AAW26610 standard; Protein: 868 AA.  
AC AAW26610;  
XX  
XX 27-JAN-1998 (first entry)  
DT  
DE Rat muscle-specific kinase (MusK).  
XX  
XX Receptor tyrosine kinase; muscle specific kinase; MusK; Dmk; rat;  
KM ligand; agrin; diagnosis; therapy.  
XX  
XX Ratius sp.  
FH  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT 1..19  
FT Domain 21..492  
FT 21..492  
FT Domain 493..521  
FT 493..521  
FT Domain 522..868  
FT 522..868  
FT Domain Intracellular\_domain  
XX  
XX WO9721811-A2.  
XX  
XX 19-JUN-1997.  
XX  
XX 13-DEC-1996; 96WO-US20696.  
XX  
XX 10-MAY-1996; 96US-0644271.  
XX  
XX 15-DEC-1995; 95US-0008657.  
XX  
XX (REGC-) REGENERON PHARM INC.  
XX  
XX Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD;  
XX  
XX WPI; 1997-332783/30.  
DR

DR N-PSDB; AAT90472.  
XX Nucleotide sequences encoding human agrin and muscle specific kinase  
PT and related receptor - used in diagnosis and treatment of disorder  
PT with muscle atrophy  
XX  
XX Example 1; Fig 1; 120pp; English.  
PS  
XX  
XX This polypeptide comprise a novel rat receptor tyrosine kinase  
CC designated muscle specific kinase (MusK) that is expressed in  
CC normal and denervated muscle. MusK is alternatively referred to  
CC Dmk for denervated muscle kinase. The amino acid sequence was  
CC deduced from an isolated cDNA clone (see AAT90472). Human MusK (see  
CC AAW26611) has also been identified. Use of MusK to generate anti-  
CC MusK antibodies and in the diagnosis of neurological or other  
CC disorders is disclosed. Assay systems that may be used to detect  
CC and/or measure ligands that bind the musk gene product are provided.  
CC A claimed method of promoting the growth, differentiation or  
CC survival of MusK receptor-expressing cells involves administration  
CC to the cell of agrin (see AAW26609). Such cells include muscle,  
CC heart, spleen, ovary and retina cells, or cells genetically  
CC engineered to express the MusK receptor.  
XX  
SQ Sequence 868 AA:

Query Match 93.9%; Score 4292.5; DB 18; Length 868;  
Best Local Similarity 93.2%; Pred. No. 0;  
Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;  
QY 1 MRELVINPLVHLITLVAFSGTEKLPKAPVITTPLETVDALEEVATFMCAYESPOPEIS 60  
DB 1 MRELVINPLVHLITLVAFSGTEKLPKAPVITTPLETVDALEEVATFMCAYESPOPEIS 60  
QY 61 WTRNKILIKLEFDRYSRENGOLITLISVEDSDGTYCCANNGYGAIVSSGALQYKMK 120  
DB 61 WTRNKILIKLEFDRYSRENGOLITLISVEDSDGTYCCANNGYGAIVSSGALQYKMK 120  
QY 121 PKITRPPINVKITIEGKAVLPCTTGNPKPSVSMIGDSPLRNSRIAYLESGLRIHNY 180  
DB 121 PKITRPPINVKITIEGKAVLPCTTGNPKPSVSMIGDSPLRNSRIAYLESGLRIHNY 180  
QY 181 QKEDAOQRCVAKNSLGTAYSKVYKLEFEYFAITLAPESHNTFSSFTVLHCTATGIPY 240  
DB 181 QKEDAOQRCVAKNSLGTAYSKVYKLEFEYFAITLAPESHNTFSSFTVLHCTATGIPY 240  
QY 241 PTTTWIENGNAVSSGSIQESVDRVIDSRLOLFTTPGTYCTATKKGKSTAAAAAT 300  
DB 241 PTTTWIENGNAVSSGSIQESVDRVIDSRLOLFTTPGTYCTATKKGKSTAAAAAT 300  
QY 301 ISTAEMSKPOKDKGYCAQYRGECNAVLAKDALVEPLNTSYADPEBAOELLVHTANNELEK 360  
DB 301 ISTAEMSKPOKDKGYCAQYRGECNAVLAKDALVEPLNTSYADPEBAOELLVHTANNELEK 360  
QY 361 VVSPVCRPAEALCNHIOECSRGVPPPIPCREYCAVKKLFFCAKKELVNEETHTHG 420  
DB 361 VVSPVCRPAEALCNHIOECSRGVPPPIPCREYCAVKKLFFCAKKELVNEETHTHG 420  
QY 421 LKSEHMLLSVPCSKLPSNHHMDPTACARLPHLDYKNENLTPPPMTSSKPSVDINPLPS 480  
DB 421 LKSEHMLLSVPCSKLPSNHHMDPTACARLPHLDYKNENLTPPPMTSSKPSVDINPLPS 480  
QY 481 SSSSSFSVSPYSMTVIISIMSSFAIFVLLTTITLTCRRRKQWKKKRSAAVTLTTLTLP 540  
DB 481 SSSSSFSVSPYSMTVIISIMSSFAIFVLLTTITLTCRRRKQWKKKRSAAVTLTTLTLP 540  
QY 541 SELLDRLHPNPMYQRMPLLNPKLLSLLEYPRNIEVVDIGGAGRGVQOARAPGLLPY 600  
DB 541 SELLDRLHPNPMYQRMPLLNPKLLSLLEYPRNIEVVDIGGAGRGVQOARAPGLLPY 600  
QY 601 EPTTMAVAVKMLKEASADQADFOREALMAEFDNPNIYKLLGVCAVGKPMCLLFEXMAY 660  
DB 601 EPTTMAVAVKMLKEASADQADFOREALMAEFDNPNIYKLLGVCAVGKPMCLLFEXMAY 660

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QY 661 GDLNEFLRSMSPHTVCSLSHSDLSMRAQVSSPGPPLSCAEOLCIAROVAAGMAYLSERK 720
Db 660 gdlneflrsmshphtvcsllshsdlsstrarvsspppplscaeqcliarqvaagmaylserk 719
QY 721 FVHRDLATRNCLVGENMNVYKIADFGLSRNISADYYKANENDAIPIRMPPESTIFYNRYT 780
Db 720 fvhrdlatrnclvgenmvvkiadfglsrnlvsadykkaqndaiplrmppestifynryt 779
QY 781 TESDVWAGVGVLMWEIFSYGLOPYGMAHEEVIYVRDGNILSCPENCPVELYNIMRLCWS 840
Db 780 tesdvwagvgvlmwelfsyglpygmaheeviyvrdgnilacpencpvelynimrlcws 839
QY 841 KLPA DRPSFTSIRILERMCE RAGTVSV 869
Db 840 klpadrpsfcsihrlqrmceraegtvgv 868

RESULT 6
AAW26507 standard; protein; 868 AA.
AAW26507;
AAW26507;
06-JAN-1998 (first entry)
Rat Dmk receptor.
Dmk receptor; tyrosine kinase receptor; signal transduction; assay;
therapy; diagnosis.
Rattus sp.
Key Location/Qualifiers
Peptide 1..19
Domain /label= Sig_peptide
Domain /label= Extracellular
Domain /label= Transmembrane
Domain /label= Intracellular

US5656473-A.
12-AUG-1997.
21-JUL-1993; 93US-0095658.
19-JAN-1995; 95US-0374834.
21-JUL-1993; 93US-0095658.
(REF-) REGENERON PHARM INC.
Rojas EA, Valenzuela DM:
WPI: 1997-414593/38.
N-PSDB: AAT87074.
New isolated human denervated muscle kinase receptor - used to
develop products for the diagnosis and treatment of neurological,
muscle or neuromuscular disorders
Example 1; Column 19-24; 31pp; English.
This polypeptide sequence comprises the rat Dmk receptor, a novel
tyrosine kinase receptor that is expressed at high levels in
denervated muscle. Its amino acid sequence was deduced from an
isolated cDNA clone (see AAT87074). Human Dmk receptor (see
AAW26506) has also been identified and can be used to develop
products for the diagnosis and treatment of neurological, muscle
or neuromuscular disorders.

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SQ Sequence 868 AA:
Query Match 93.9%; Score 4292.5; DB 18; Length 868;
Best Local Similarity 93.28; Pred. No. 0;
Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

QY 1 MRELNIPLVHILVAFSGTEKLPKAPVITTPLEVDALVEEVPFMAVESYPOPEIS 60
Db 1 mrelniplvhlvafsgteklpkapvittplevdalveevpfmavesypopeis 60
QY 61 WTRNKILIKLPDRYSIRENGQILITLSEDSDDGICCTANNGVGAVSCGMLQYKMK 120
Db 61 wtrnkililikpdrysirengqililtsvedsdgicyctanngvgavscgalmqyk 120
QY 121 PKITRPPINVKIIEGLKAVIPCTTMGNPKPSVSIKGDSPLEKRSRIAVLESGLRIHNV 180
Db 121 pkitrppinvkiliegllkavipcttmgnpkpsvsiikgdsplerkrsriavlesg 180
QY 181 QKEDAGQYRCVAKNSLGTAVSKVYKLEFEVFARILRAPESHNTFGSEFVTLHCTATGIPV 240
Db 181 qkedagqyrcvaknslgtavskvyklefevfartilrapeshntfgsefvtlhctatg 240
QY 241 PTTWIENGNAVSSGSIQESYKDRVIDSRLOLFTTKGCLTCTATNKGFEFTAKAAT 300
Db 241 pttwiengnavssgsiqesykdrvidsrlolfttkgcltctatnkgfeftakaa 300
QY 301 ISIAEMSKPOKDNKGYCAOYRGEVCNVAFLKDALVFINTSYADPEEAQOELVHTAMNKL 360
Db 301 isiaemskpokdnkgycaoyrgevcnvaflkdalvfintsyadpeeaqoelvhtam 360
QY 361 VSPFCRPAEALLCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKEMLVMEKTHRG 420
Db 361 vspfcrpaeeallcnhifqecspgvvptpipcreyclavkelfcakemlvmeekth 420
QY 421 LYRSEMLISVPRKSKLPMSHMDPTACARLPHLDYKNENKTFPPMSSKRSVDIPILPS 480
Db 421 lyrsesmlisvprksklpmsmmdptacarlp hldyknentfppmsskrsvdipil 480
QY 481 SSSSFSVSPPTYSMTVLIISMSFAIFVLITITLYCCRRKQKNNKRESAAVTLTLP 540
Db 480 astsfavspaysmtvliismscfavfallitltyccrrrkqknnkresaaavl 540
QY 541 SELLDRLHPNMYQRMPLINPKLSLEYPRNNIEYVDIGEGAFGRVFOARPGILPY 600
Db 540 sellldrlhpnmyqrmpllnpklsleyprnnieyvdigegafgrvfoarpgilpy 600
QY 601 EPTMVAVKMKKEASADMOMDROREALMAEPNPNIYKLGCAVGKPMCLFEFYAY 660
Db 600 eptmvavkmkkeasadmomdrorealmepnpniykgcavgkpmclfeeymay 660
QY 661 GDLNEFLRSMSPHTVCSLSHSDLSMRAQVSSPGPPLSCAEOLCIAROVAAGMAYLSERK 720
Db 660 gdlneflrsmshphtvcsllshsdlsstrarvsspppplscaeqcliarqvaagmayls 719
QY 721 FVHRDLATRNCLVGENMNVYKIADFGLSRNISADYYKANENDAIPIRMPPESTIFYNRYT 780
Db 720 fvhrdlatrnclvgenmvvkiadfglsrnlvsadykkaqndaiplrmppestify 779
QY 781 TESDVWAGVGVLMWEIFSYGLOPYGMAHEEVIYVRDGNILSCPENCPVELYNIMRLCWS 840
Db 780 tesdvwagvgvlmwelfsyglpygmaheeviyvrdgnilacpencpvelynimrlcws 839
QY 841 KLPA DRPSFTSIRILERMCE RAGTVSV 869
Db 840 klpadrpsfcsihrlqrmceraegtvgv 868

RESULT 7
AAW2717 standard; protein; 868 AA.
AAW2717;

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XX 27-MAY-1996 (first entry)  
 DT Mouse muscle-localised protein-tyrosine-kinase receptor-2 isoform.  
 XX  
 DE Mouse muscle-localised protein-tyrosine-kinase receptor-2 isoform;  
 XX mlk-2; treatment; monoclonal antibody; receptor ligand;  
 KW receptor-antagonist; muscular dystrophy; familial dysautonomia;  
 KW congenital myopathy; myotonia congenita; myasthenia gravis;  
 KW familial periodic paralysis; Eaton Lambert syndrome;  
 KW paroxysmal myoglobinuria; secondary myasthenia;  
 KW denervation atrophy; nervous system disease; vascular disorder;  
 KW trauma; metabolic derangement; multiple sclerosis; epilepsy;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;  
 KW amyotrophic lateral sclerosis; primary lateral sclerosis;  
 KW Merinig-Hoffman disease; syringomyelia; peripheral neuropathy;  
 KW congenital anomaly; tumor.  
 XX  
 OS Mus musculus.  
 XX  
 FH Location/Qualifiers  
 FH Peptide  
 FT 1..21  
 FT /note= "mlk-2 protein signal peptide"  
 FT Domain  
 FT 22..462  
 FT /note= "soluble mlk-2 domain"  
 FT 22..494  
 FT /note= "soluble mlk-2 domain"  
 FT Domain  
 FT 22..494  
 FT /note= "mlk-2 protein extracellular domain"  
 FT 495..515  
 FT /note= "mlk-2 protein transmembrane domain"  
 FT Domain  
 FT 516..868  
 FT /note= "mlk-2 protein intracellular domain"  
 FT 580..855  
 FT /note= "mlk-2 protein-tyrosine-kinase domain"  
 FT  
 XX  
 PN WO9602644-A1.  
 XX  
 PD 01-FEB-1996.  
 XX  
 PF 06-JUL-1995; 95WO-US08493.  
 XX  
 PR 01-FEB-1995; 95US-0384710.  
 PR 20-JUL-1994; 94US-0277803.  
 XX  
 PA (GENY ) GENETICS INST INC.  
 XX  
 CA Caruso A, Wood C;  
 XX  
 DR WPI: 1996-105906/11.  
 DR N-PSDB: AAT16349.  
 XX  
 PT DNA encoding 'muscle-localised kinase' family of receptor tyrosine  
 PT kinase(s) - also receptor ligands, antibodies and inhibitors,  
 PT useful for promoting or inhibiting bone or cartilage growth or bone  
 PT loss.  
 XX  
 PS Claim 14: Page 71-73; 89pp; English.  
 XX  
 CC Recombinantly produced mouse muscle-localised protein-tyrosine  
 CC kinase receptor-2 isoform (mlk-2) may be used to identify and  
 CC isolate mlk-2 binding ligands, or to screen for agents capable of  
 CC binding to mlk-2 protein, which may act as inhibitors of normal  
 CC ligand binding. Isolated mlk-2 and mlk-2 receptor ligands may be  
 CC useful in the treatment of various medical conditions including  
 CC muscle-related disorders, nervous system diseases, vascular  
 CC disorders, trauma, metabolic derangements, demyelinating diseases,  
 CC epilepsy, neuronal disease including motor neuron diseases,  
 CC syringomyelia, peripheral neuropathy, congenital anomalies and  
 CC tumors. Isolated mlk-2 protein may also be used to immunize  
 CC animals to obtain polyclonal and preferably monoclonal antibodies,  
 CC which specifically react with mlk-2 and which may inhibit ligand  
 CC binding to the receptor. These antibodies may be used as

CC therapeutics for certain tumors and in the treatment of the above  
 CC mentioned conditions. Smaller mlk fragments may be used to  
 CC immunize animals.

XX Sequence 868 AA:

Query Match 93.4%; Score 4269.5; DB 17; Length 868;  
 Best Local Similarity 92.9%; Pred. No. 0;  
 Matches 807; Conservative 30; Mismatches 31; Indels 1; Gaps 1;

QY 1 MRLVNIPIVHILITLVAESGTEKLRKAPVITPTLETVDALVEEVATFMCVAVESPPPEIS 60  
 DB 1 mrlvniplvhlitlvaesgteklrkavipcttmgnpkpsvslgdnalrenstlavlesgslthnv 180  
 QY 61 WTRNKLLIKLFDTRYISRENGQLLTLSVEDSDGTYCCTANNVGAVESGALOVKMK 120  
 DB 61 wtrnklliklfdtryisrengqltltsvedsdgtyccianngvgavescgalqvkmk 120  
 QY 121 PKITRPINKITIEGKAVIPCTTMGNPKPSVWIKGDSPLRENSRLAVESGLRTHNV 180  
 DB 121 pkitrpinvkliegkavipcttmgnpkpsvslgdnalrenstlavlesgslthnv 180  
 QY 181 QKEDAGQYRCVAKNSLGTAVSKVVKLEFEVFARILRAPESHNTFGSFYTLHCTATGIPV 240  
 DB 181 qkedagqyrcvaksnglgtavskvkvlefevfartilrapeshntfgsfylrctalgipv 240  
 QY 241 PTTTNIENGNVAVSSGSIQESVYKRVIDSRLQLFTTPRGLYTCATNKGKSTAKAAT 300  
 DB 241 ptttniengnvavssgsiqesvkvrvidsrlqlfttkpgrlytcatnkhgkfstakaaat 300  
 QY 301 ISIAEWSKPOKDNKGYCAQYRGVCNANVLAKDALVFNLTSTADPEEAQELVHTANNEIK 360  
 DB 301 isiaewskpokdnkgycaqyrgvcnnavlakdalvfnltstadepeeaqelvtananelk 360  
 QY 361 VSPVCRPAEALLCNHIFQECSPGVVPPPIPCREYCLAVALFCAKEWLVNEERTHRG 420  
 DB 361 avspcrpaeeallcnhlfecspgvvpmpipcreyclavalfcawkewlvneertkhr 420  
 QY 421 LYRSEMHILSVKCSKLPKSHMHPDTCARLPHIDYKKNKLTTPMTSSSPVDIPLPS 480  
 DB 421 lyrsemhilsvkcsklpksmhpdpctcarlphidykknklttppmtssspvdiplps 480  
 QY 481 SSSSEFSVSEPTYSMTVLIISMSFAIFVLTTITLCCRRRKQMKKKRESAATVLTTLTP 540  
 DB 481 ssssefsvseptysmvtliismsfaifvlttittlccrrrkqmkkkresaatvlttltp 540  
 QY 480 aasfsefvapaysmvtliisvsefalfaltltyccrrrkewkhhkrestavlttltp 539  
 QY 541 SEILLDLRLHPNMYQRMPLLNPKLLSLEYPRNNIEYVRDIGEGARGVFQARAPGLPY 600  
 DB 540 seilldlrlhpnmyqrmpllnpkllsleyprnnieyvrDIGEGARGVFQARAPGLPY 599  
 QY 601 EPTTWAVKMKLEASADQADQFORALMAEDNDNIVKLVGCAVGRKMLCFEYMAT 660  
 DB 601 epttwavkmlkeasadqadqforalmaedndnivkvgcavgrkmlcfeymay 659  
 QY 661 GDINEFLRSKSPHTVCSLSHSDLSMRBOVSSPPPLSCAQECIRQVAVAGAAVYSERK 720  
 DB 660 gdineflrsksphtvcsllshsdlsmrbovssppplscaqecirqvavaagmayiserk 719  
 QY 721 FVHRDLATRNCLGVEMVVKIADFGLSRNITYSADYYKANENDAIPIRMMPESIFYNRYT 780  
 DB 721 fvhrdlatrnclgvemvVKIADFGLSRNITYSADYYKANENDAIPIRMMPESIFYNRYT 779  
 QY 781 TESDWAAGVGVLMETISYGLQPYGMAHEVITYVVDGNTLSPENCQVETLYMLMLCWS 840  
 DB 780 tesdwaagvgvlmetsyglqpygmahevityvvdgnllacpencqetlymlmlcws 839  
 QY 841 KLFPADRPSTSIHRIERMCEARECTVSV 869  
 DB 840 klpadrpsstsihrlirmcearegtvsv 868

RESULT 8

AAR92716  
 ID AAR92716 standard; protein; 860 AA.  
 AC AAR92716;  
 DT 04-JUN-1996 (first entry)  
 XX  
 DE Mouse muscle-localised protein-tyrosine-kinase receptor-1 isoform.  
 XX  
 KW Mouse muscle-localised protein-tyrosine-kinase receptor-1 isoform;  
 KW treatment; monoclonal antibody; receptor ligand;  
 KW receptor-antagonist; muscular dystrophy; familial dysautonomia;  
 KW congenital myopathy; myotonia congenita; myasthenia gravis;  
 KW familial periodic paralysis; Eaton-Lambert syndrome;  
 KW paroxysmal myoglobinuria; secondary myasthenia;  
 KW denervation atrophy; nervous system disease; vascular disorder;  
 KW trauma; metabolic derangement; multiple sclerosis; epilepsy;  
 KW Alzheimer's disease; Parkinson's disease; Huntington's chorea;  
 KW amyotrophic lateral sclerosis; primary lateral sclerosis;  
 KW Merdidi-Hoffman disease; syringomyelia; peripheral neuropathy;  
 KW congenital anomaly; tumor.  
 XX  
 MS Mus musculus.  
 XX  
 FH Key  
 FT Peptide  
 FT 1..21  
 FT /note= "mlk-1 protein signal peptide"  
 FT 22..453  
 FT /note= "soluble mlk-1 domain"  
 FT 22..486  
 FT /note= "soluble mlk-1 domain"  
 FT 22..486  
 FT /note= "mlk-1 protein extracellular domain"  
 FT 487..507  
 FT /note= "mlk-1 protein transmembrane domain"  
 FT 508..860  
 FT /note= "mlk-1 protein intracellular domain"  
 FT 572..847  
 FT /note= "mlk-1 protein-tyrosine-kinase domain"  
 XX  
 PN MO9602644-A1.  
 PD 01-FEB-1996.  
 XX  
 PF 06-JUL-1995; 95WO-US08493.  
 XX  
 PR 01-FEB-1995; 95US-0384710.  
 PR 20-JUL-1994; 94US-0277803.  
 XX  
 (GENY ) GENETICS INST INC.  
 PI Caruso A, Wood C;  
 XX  
 DR WPI, 1996-105906/11.  
 DR N-PSDB; AAT16348.  
 XX  
 PT DNA encoding 'muscle-localised kinase' family of receptor tyrosine  
 PT kinase(s) - also receptor ligands, antibodies and inhibitors,  
 PT useful for promoting or inhibiting bone or cartilage growth or bone  
 PT loss.  
 XX  
 PS Claim 14; Page 64-67; 89pp; English.  
 XX  
 CC Recombinantly produced mouse muscle-localised protein-tyrosine  
 CC -kinase receptor-1 isoform (mlk-1) may be used to identify and  
 CC isolate mlk-1 binding ligands, or to screen for agents capable of  
 CC binding to mlk-1 protein, which may act as inhibitors of normal  
 CC ligand binding. Isolated mlk-1 and mlk-1 receptor ligands may be  
 CC useful in the treatment of various medical conditions including  
 CC muscle-related disorders, nervous system diseases, vascular  
 CC disorders, trauma, metabolic derangements, demyelinating diseases,  
 CC epilepsy, neuronal disease, including motor neuron diseases,  
 CC syringomyelia, peripheral neuropathy, congenital anomalies and

CC tumours. Isolated mlk-1 protein may also be used to immunize  
 CC animals to obtain polyclonal and preferably monoclonal antibodies,  
 CC which specifically react with mlk-1 and which may inhibit ligand  
 CC binding to the receptor. These antibodies may be used as  
 CC therapeutics for certain tumors and in the treatment of the above  
 CC mentioned conditions. Smaller mlk fragments may be used to  
 CC immunize animals.  
 CC  
 XX  
 SQ Sequence 860 AA;  
 Query Match 92.4%; Score 4220.5; DB 17; Length 860;  
 Best Local Similarity 92.2%; Pred. No. 0;  
 Matches 801; Conservative 29; Mismatches 30; Indels 9; Gaps 2;  
 QY 1 MRELVIPLVHILTLVAFSGTEKLPKRPVITPLEYTDALVEEATMCAVESYPOEIS 60  
 DB 1 mrelvnpilqlmltlvafsgteklpkapvltpleytdalveeatmcavesyppois 60  
 QY 61 WTRKKILIKLFDPFRYSIRENGQLTLTISVEDSDGICCTANNVGAVSCGALQYKMK 120  
 DB 61 wtrnkliklfdfrysirengqltltsvedsdgicyclannvgavscgalykkmk 120  
 QY 121 PKITRPPINVKIIEGLKAVLPCTTMGNPKDSVSNIKDPSIRENSRIAVLESGSLRTINV 180  
 DB 121 pkitrppinvklliegikavlpcttmgnpkpsvswikgdnairensriavlesgslrhv 180  
 QY 181 OKEDAGYRCVAKNSLTCTAASKYVKLEFEVFARILRPESHNVFGSFVTLHCATGIPV 240  
 DB 181 qkedaagyrcvaknsltctaaakskvklvleevfarilrpesnhvfgsfvtlrcacaiipv 240  
 QY 241 PPTWIENGNAVSSGSIOESYKRDVIDSRQLFTTKRGLYTCIATNKGKSTAKAAT 300  
 DB 241 ptlswiengnavssgsiqesvkdvdidsrlqflftkpglytciatnkgkfstakaat 300  
 QY 301 ISTAEKSPQKDKNGYCAOTRGEYCNAYLAKDALVFINTSYADEEAOELLHTANMEIK 360  
 DB 301 istaewksqkdsqgycaoyrgevcadavlakdalvfintsyrdpedaqellihawelk 360  
 QY 361 VVSPVCPRAAEALCNHIFECSSGVVPTPIPCIREYCLAVKELFCKEWLVMEKTHRG 420  
 DB 361 avspjcrpaaeallcnhlfecssgvvptpmpicireyclavkelfckewmgamgkhr 420  
 QY 421 LYRSEMLLSVPKCSKLPSMHWDEPTACARLPHLDYKNENLTPPMTSKPSVDIPMPS 480  
 DB 421 lyrsghmllypvecsklpsmhwdptacarlphldyknenktpmmtskpsvdipmhp 471  
 QY 481 SSSSFVSVPYSMTVLIISMSFAIFVLITTLTGCRRRKOKNKKRESAATLTLP 540  
 DB 472 astsfavspysmtvliisvstalfalltlalylccrrtkewknkkrstavlcltlp 531  
 QY 541 SELLDRLHNPMTQRMPLLLNPKLLSLEYVRNNIEYVRDIGEAGFGRVQARAGLLPY 600  
 DB 532 sellldrlhnpmpyrmpillnplkllsleyvrnnieyvrDIGEAGFGRVQARAGLLPY 591  
 QY 601 EPTTVAVKMLKEBASDMQADFOREALAIAEPNPINIKILGYCAYGKPMCLLFETMAX 660  
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 QY 661 GDINEFLRSMSPHNYCSLISHDSLMSRAOVSSPGPPISCAEQLCIAOVAAGMAYLSERK 720  
 DB 652 gdineflrsmshnycslishdsldstravsspppilscaeqclatqvaagmaylserrk 711  
 QY 721 FVHRDLATRNCLVGENNVKLTADFLSRNTYSADYRYANENDALPIRMMPESIFYNRYT 780  
 DB 712 fvhrdlatrncclvgenmvkltadflsrnysadyryadgdaiprlwmpesifynryt 771  
 QY 781 TESQVWYGVVWLEIFSYGIOPYGMAHEVITYYVRGNILSCBENCPVELYNMRKCS 840  
 DB 772 tesqvwygvvwlwelfsygiopygmaheviyyvrgnilscbenpvelynmrkcs 831  
 QY 841 KLPRDRPSFTSIHRLERMCRACGTSVY 869  
 DB 841 klprdrpsftsihrlermcracgtsvy 869



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|||||
Db 777 fyrrytesvayvylwifsgylqpygmahewiyyvridgnllacpenopllynl 836
QY 835 MRLCWSKLPADRPSTSIHRIERMCERAEQVSV 869
Db 837 mrlcwsklpadrpsfcsihrlqmceraegtygv 871

RESULT 10
AAW62568
ID AAW62568 standard; Protein, 871 AA.
XX
AC AAW62568;
XX
DT 12-OCT-1998 (first entry)
XX
DE Mouse receptor tyrosine kinase Nsk2.
XX
KW Nsk2; Nsk-2; neural fold/somite kinase 2; receptor tyrosine kinase;
KW mouse; signal transduction; tumour; cancer; neuromuscular disease;
KW muscle; muscular dystrophy.
XX
MS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= Sig_peptide
FT /note= "Claim 8"
FT Protein 22..871
FT /label= Mat_protein
FT Region 22..496
FT /label= Extracellular
FT /note= "Claim 8"
FT 49..98
FT /label= Ig_like
FT /note= "Claim 8"
FT 233..282
FT /label= Ig_like
FT /note= "Claim 8"
FT 401..450
FT /label= Ig_like
FT /note= "Claim 8"
FT Modified-site 222..224
FT /note= "Asn is N-glycosylated"
FT 462..464
FT /note= "Asn is N-glycosylated"
FT 497..517
FT /label= Transmembrane
FT /note= "Claim 8"
FT 518..871
FT /label= Intracellular
FT /note= "Claim 8"
FT 518..576
FT /label= Juxtamembrane
FT 577..858
FT /label= Tyrosine-kinase
FT /note= "Claim 8"
FT 674..693
FT /label= Kinase_insert
FT /note= "Claim 8"
FT 859..871
FT /label= Carboxy_terminal
FT /note= "Claim 8"
FT Misc-difference 25
FT /note= "encoded by CCN"
XX
PN W09820114-A1.
XX
PD 14-MAY-1998.
XX
PF 29-OCT-1997; 97MO-US19646.
XX
PR 07-NOV-1996; 96DS-0737855.

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XX
PA (LUDW-) LUDWIG INSR CANCER RES.
XX
PI Reith A, Ruegg M;
XX
DR WPI; 1998-286930/25.
XX
DR N-PSDB; AAV38546.
XX
PT Muscle receptor tyrosine kinase, Nsk2, or its alternatively spliced
PT isoforms - useful for inhibiting receptor tyrosine kinase signalling
PT pathways and tumour development
XX
PS Claim 7; Fig 2; 110pp; English.
XX
CC This polypeptide comprises a novel muscle receptor tyrosine kinase
CC (RTK) designated Nsk2 (neural fold/somite kinase). Its amino acid
CC sequence was deduced from a mouse skeletal myotube cDNA clone (see
CC AAV38546). Various alternative isoforms (see AAW62569-77) of Nsk2
CC have been identified that result from differential splicing of the
CC Nsk2 transcription unit. The invention provides expression vectors,
CC transformed or transfected host cells, a monoclonal antibody, a
CC related RTK designated Nsk1 (see AAV38551), and the following methods:
CC (a) screening for a neuromuscular disease (ND) by comparing the
CC levels of RTK from a sample and a control, where a difference is
CC indicative of ND; (b) monitoring the progression or regression of ND
CC by comparing the levels of RTK from a patient at different times, and
CC (c) determining the efficacy of a therapeutic agent in the treatment
CC of ND by comparing the levels of RTK prior to, and post-administration,
CC and differentiation of mammalian skeletal myotubes. Antibodies to
CC the protein are especially useful for inhibiting signal pathways
CC involving muscle RTKs and thus can be used to inhibit tumour
CC development.
XX
SQ Sequence 871 AA;
XX
Query Match 90.58; Score 4136; DB 19; Length 871;
Best Local Similarity 90.3%; Pred. No. 0;
Matches 790; Conservative 30; Mismatches 45; Indels 10; Gaps 4;
QY 1 MRELVINPIVHILFLVAFSGTERLPRKAVITPTPEYDALVEEATMCAVESPOPEIS 60
Db 1 mrelvinpilmvlfaifsgteklpprvlatpjetdaveeatlmcavespppeis 60
QY 61 WTRNKILIKLEFDTRYRSIRENGQLTILSVESDDGIVCYCTANNVGAVESGALQYKMK 120
Db 61 wtrnkililklfdtryrsirengqltllsvedsdgivccianngvgavesgalykkm 120
QY 121 PKITRPPINVKIIEGLKAVLPCTTMGNPKPSVSIKGDSPREMSRIAYLESGSLRIHN 180
Db 121 pkitrppinvklliegkavlpctltmgnpkpsvswkqdnalrensrilaalsgslrlhnv 180
QY 181 QKEDAGQRCYAKNSLGTAYSVKVLFEFVAFARILRPESHNVTFGSEFVLHCTATGIPV 240
Db 181 qkedagqrcvaknslgtayskvvlfeefvafarilrpeshnvtfgsfvlrlcteiqiv 240
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Db 241 pttwiengnavssgsioesykdrvidsrllftlkpglylciaitnkgefstakaaat 300
QY 301 ISTAEWSKPOKDNKGCAQYRGVECNMVL----AKDALVFL-NTSYADPEAOELLVHT 354
Db 301 vsiaewskqkdsqgycqdyrge---gvlmggpgekmlvflptshndpdaqelllht 357
QY 355 AMNELKVVSPYCPRAAEALCNHIFOECSPGVVPPIPICREYCLAVKELCAKEWLME 414
Db 358 amnelkavspicrpaaeallcyhflflecspgvvpmpicreyclavkelcakewame 417
QY 415 EKTIRGLYRSEMHLLSVPKCSLPSMHWDPACARLPHLDYKNKNLKTPEPMTSKPSVD 474
Db 418 gkahrtylrsqmhllpvepcrkllpsmhndpactrlpyldykkenitlftpsltsrpsad 477

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QY 475 IPNIPSSSSSESVSPYISMTVIISIMSSFAIFVLITTLTLYCCRRRKQKKNKRESAAV 534
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Db 478 ipnlp-satsfavsfpysmtvlisvslalfallclivclccrrrkewknkrestav 536
QY 535 TLTLPSELLELDRLHPRWQRMPLLNPKLLSEYPRNNIEYRDIGEGAFGVFPARA 594
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 537 cltlpseellldrlhprwqrmpllnpkllseypnnlseyrdigegafigrvfgara 596
QY 595 PGLLPYEPFTMVAVKMLKEESADQMADFOREALMAEFDPNPVTKLIGCAVCKPKPCLL 654
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Db 597 pgllypepfcmvavkmlkeesasdmqdfqreaalmeefdnplvkllygcaavgkpmcll 656
QY 655 PEYWAYDLEPLRSMSPHTVCSLSHSDLSMAQVSSGPPEPLSCABQLCIARQVAAGMA 714
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Db 717 ylsrkfvhrdlatrncldvgenwvkvadfglsknitlsadyikanendaipirmpest 776
QY 775 FYNRYTSEDVMAVGVYLMETFSYGLQPYGYGMAHEEYIYVRDGNILSCPCNPVELYNL 834
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Db 777 fyntytesdvavgvylmetfsglyqipygygmaheeyiyvrngnllacpcnplaynl 836
QY 835 MRLCWSKLPADRPSEFSIHRLERMCEERAGTYSV 869
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Db 837 mrlcwsklpadrpsfscshrlqrmceragetygv 871

RESULT 11
ID AAM62572 standard; Protein; 881 AA.
AC AAM62572:
XX
XX
DT 12-OCT-1998 (first entry)
XX
DE Mouse Nsk2 (alternatively spliced isoform).
XX
XX Nsk2; Nsn-2; neural fold/somite kinase 2; receptor tyrosine kinase;
KW mouse; signal transduction; tumour; cancer; neuromuscular disease;
XX muscle; muscular dystrophy.
XX
OS Mus sp.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /label= Sig-peptide
FT 22..871
FT /label= Mat-protein
FT Region 22..496
FT /label= Extracellular
FT Domain 49..98
FT /label= Ig-like
FT 233..282
FT /label= Ig-like
FT Domain 401..450
FT /label= Ig-like
FT 222..224
FT /note= "Asn is N-glycosylated"
FT Modified-site 462..464
FT /note= "Asn is N-glycosylated"
FT Domain 497..517
FT /label= Transmembrane
FT Region 518..881
FT /label= Intracellular
FT Domain 518..576
FT /label= Juxtamembrane
FT Domain 577..858
FT /label= Tyrosine-kinase
FT Domain 674..693
FT /label= Kinase_insert
FT 859..881
FT Domain

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FT /label= Carboxy_terminal
PN W09820114-A1.
XX
XX 14-MAY-1998.
XX
XX 29-OCT-1997; 97MO-US19646.
XX
XX 07-NOV-1996; 96US-0737855.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Reith A, Ruegg M;
XX
XX WPI; 1998-286930/25.
XX
XX Muscle receptor tyrosine kinase, Nsk2, or its alternatively spliced
PT isoforms - useful for inhibiting receptor tyrosine kinase signalling
PT pathways and tumour development
XX
XX Claim 1; Fig 4b; 110pp; English.
XX
XX This polypeptide comprises an isoform of a novel muscle receptor
CC tyrosine kinase (RTK) designated Nsk2 (neural fold/somite kinase)
CC (see also AAM62568) bearing an alternatively spliced C-terminal
CC domain (see also AAM62571). This isoform is produced in mouse foetal
CC myotube clones. Various alternative isoforms (see AAM62569-77) of Nsk2
CC have been identified that result from differential splicing of the
CC Nsk2 transcription unit. The invention provides expression vectors,
CC transformed or transfected host cells, a monoclonal antibody, a
CC related RTK designated Nsk1 (see AAV38551), and the following methods:
CC (a) screening for a neuromuscular disease (ND) by comparing the
CC levels of RTK from a sample and a control, where a difference is
CC indicative of ND; (b) monitoring the progression or regression of ND
CC by comparing the levels of RTK from a patient at different times, and
CC (c) determining the efficacy of a therapeutic agent in the treatment
CC of ND by comparing the levels of RTK prior to, and post-administration,
CC of the agent. The Nsk2 gene sequence can be used to study the growth
CC and differentiation of mammalian skeletal myotubes. Antibodies to
CC the protein are especially useful for inhibiting signal pathways
CC involving muscle RTks and thus can be used to inhibit tumour
CC development.
XX
XX
SQ Sequence 881 AA;
XX
XX
Query Match 90.3%; Score 4128; DB 19; Length 881;
Best Local Similarity 90.4%; Pred. No. 0;
Matches 788; Conservative 30; Mismatches 44; Indels 10; Gaps 4;
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Db 1 mreivnlpilgmlltvaifsteklppvyaqlpvevdalvevatfmcavesypqets 60
QY 61 WTRNKLILKLFDTIRYSIRENGQLLTLLSYEDSDDGICYCTANNGVGAVERSCALGVKMK 120
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Db 61 wtrnklllkfldtryisirengqltllsyedsddgyccclanngvgavescalgvkmk 120
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QY 181 OKEDAGQYRCVANKSLGTAYSKVVKLEFVFAIRILRAPSHNVTFGSFYTLCTATGIPV 240
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Db 181 qkedagqyrcvankslgtayskvklrevvlgriilapeshnvtfgsfylctctelgipv 240
QY 241 PIIITWENGNAVSSGSIQGSVKDRIYDSRLQLEPIKGLYTCIATANKHGEKFSATAAAT 300
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Db 241 piiitwengnavssgsiqgsvkdrivdsrlqlfitykpylytclatnkhekfstakaat 300
QY 301 ISIAEWSKPOKXKNGYCAQYRGECVNAVL-----AKDALVFL-NMSYADPEEAQELLVHT 354
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 vsiaewsksqkdsqycqdyrge---gvimqpgpexkmlivflptcshtdpedagellht 357

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OY 121 PKTRPPIVKIIIEGLKAVLPCTTMGNPKPSVSIKGDSPLENSRIATVLESGSLRIHNV 180
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OY 181 QKEDACQYRCVANKSLGTAVSKVYKLEFEVFARILRAPESHNVFGSFVTLHCTATGIPV 240
DB 181 QKEDACQYRCVANKSLGTAVSKVYKLEFEVFARILRAPESHNVFGSFVTLHCTATGIPV 240
OY 241 PRTTWIENGNAVSSGSIQSVKVDISRLQFLITRKGLYTCTATNKGKSTAKAAAT 300
DB 241 PRTTWIENGNAVSSGSIQSVKVDISRLQFLITRKGLYTCTATNKGKSTAKAAAT 300
OY 301 ISIAEMSKPOKDNKGYCAQYRGECNAVL-----AKDAVFL-NTSYADEEAOELLVHT 354
DB 301 ISIAEMSKPOKDNKGYCAQYRGECNAVL-----AKDAVFL-NTSYADEEAOELLVHT 354
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DB 475 IRLPSSSSSSFSVSPFTYMTVSIISMSFAIFVLLTITLYCCRRRQMKMKKRESAAV 534
OY 535 TLTTLPSSELLDRHPNPNYORMPILLNPKLSLEYPNNIEYVRIGGAGRVQANA 594
DB 535 TLTTLPSSELLDRHPNPNYORMPILLNPKLSLEYPNNIEYVRIGGAGRVQANA 594
OY 595 PCLLPYEPETMAVVKMLKEASADMDQADFORBAALMAEFNDPNIVKLVCAVGRPMCL 654
DB 595 PCLLPYEPETMAVVKMLKEASADMDQADFORBAALMAEFNDPNIVKLVCAVGRPMCL 654
OY 655 FEYMAVYGDLEFRLRSPTVCSLSHSDLSMAQVSSPEPPLSCAEQLCIRQVAAAGMA 714
DB 655 FEYMAVYGDLEFRLRSPTVCSLSHSDLSMAQVSSPEPPLSCAEQLCIRQVAAAGMA 714
OY 715 YLSERKFVHRDLATRNCLGVENNVKADFGLSRNYSADYKANKENDAIPIRWMPPESI 774
DB 715 YLSERKFVHRDLATRNCLGVENNVKADFGLSRNYSADYKANKENDAIPIRWMPPESI 774
OY 775 FVNRTTESDVAVGVVMEIRFSTGLQPYGMAHEEVIVYVDGNILSCPENCPVELYNL 834
DB 775 FVNRTTESDVAVGVVMEIRFSTGLQPYGMAHEEVIVYVDGNILSCPENCPVELYNL 834
OY 835 MRLCWSKLPADRPFTSIHRILERMCEPACETVSV 869
DB 835 MRLCWSKLPADRPFTSIHRILERMCEPACETVSV 869
OY 869 MRLCWSKLPADRPFTSIHRILERMCEPACETVSV 869
DB 869 MRLCWSKLPADRPFTSIHRILERMCEPACETVSV 869

RESULT 15
AAW62573
ID AAW62573 standard; Protein: 873 AA.
XX
AC AAW62573:
XX
DT 12-OCT-1998 (first entry)
XX
DE Alternatively spliced mouse receptor tyrosine kinase Nsk2.
XX
KW Nsk2; Man-2; neural fold/somite kinase 2; receptor tyrosine kinase;
KW mouse; signal transduction; tumour; cancer; neuromuscular disease;
KW muscle; muscular dystrophy.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= sig_peptide

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FT Protein 22..863
FT /label= Mat_protein
FT Region 22..488
FT /label= Extracellular
FT Domain 49..98
FT /label= Ig-like
FT Domain 142..190
FT /label= Ig-like
FT Domain 233..282
FT /label= Ig-like
FT Modified-site 222..224
FT /note= "Asn is N-glycosylated"
FT Domain 489..509
FT /label= Transmembrane
FT Region 510..873
FT /label= Intracellular
FT Domain 510..568
FT /label= Juxtamembrane
FT Domain 569..850
FT /label= Tyrosine_kinase
FT Domain 666..685
FT /label= Kinase_insert
FT Domain 851..873
FT /label= Carboxy_terminal

MO9820114-A1.
14-MAY-1998.
29-OCT-1997; 97WO-US19646.
07-NOV-1996; 96US-0737855.
(LUDW-) LUDWIG INST CANCER RES.
Reith A, Ruegg M:
WPI: 1998-286930/25.
Muscle receptor tyrosine kinase, Nsk2, or its alternatively spliced
isoforms - useful for inhibiting receptor tyrosine kinase signalling
pathways and tumour development
Claim 7: Fig 4c; 110pp; English.
XX
XX This polypeptide comprises an alternatively spliced isoform of
XX a novel mouse muscle receptor tyrosine kinase (RTK) designated Nsk2
XX (neural fold/somite kinase) (see also AAW62568). A deletion of 24
XX nucleotides (1415-1438) of Nsk2 cDNA (see AAV38546) results in
XX replacement of aa457-465 of Nsk2 with a single alanine residue,
XX while further alternative splicing alters the C-terminal sequence
XX (see also W625710). This isoform is expressed in foetal myotubes.
XX Various alternative isoforms (see AAW62569-77) of Nsk2 have been
XX identified that result from differential splicing of the Nsk2
XX transcription unit. The invention provides expression vectors, a
XX transformed or transfected host cells, a monoclonal antibody, a
XX related RTK designated Nsk1 (see AAV38591), and the following methods
XX for: (a) screening for a neuromuscular disease (ND) by comparing the
XX levels of RTK from a sample and a control, where a difference is
XX indicative of ND; (b) monitoring the progression or regression of ND
XX by comparing the levels of RTK from a patient at different times, and
XX (c) determining the efficacy of a therapeutic agent in the treatment
XX of the agent. Antibodies to the protein are useful for inhibiting
XX signal pathways involving muscle RTKs and thus can be used to
XX inhibit tumour development.
SQ Sequence 873 AA;

```

Query Match 89.3%; Score 4079; DB 19; Length 873;  
 Best Local Similarity 89.7%; Mismatches 43; Indels 18; Gaps 5;  
 Matches 782; Conservative 29;

QY 1 MRELVINPLVHILTLVAFSCTEKLPRAPVITPPLTVDALVEEVAFPMAVESYPOPEIS 60  
 Db 1 mrelvinplilqmtlvaafsfsteklpkxpvatpletvdaiveevalfmcavesypqpeis 60  
 QY 61 WTRNKILIKLPDTRYSIRENGOLTLISVEDSDGTYCCCTANNNGVGAVERSCALQYKMK 120  
 Db 61 wtrnkiliklfdtrysirengqlltlisvedsddgtyccclannngvgavaesgcalqykmk 120  
 QY 121 PKITRPPINKITEGLKAVJPCCTTMGNPKPSVSMIKGDSPLRENSRIAVLESGLRIHNV 180  
 Db 121 pkitrppinkiteglkavjpccttmgnpkpsvsmikgdsplrensrivalesgslrihmv 180  
 QY 181 QKEDAGQYRCVANKSLGTAVSKVVKLEFEVAPARILRAPESHNTFGSEVTLHCTATGIPY 240  
 Db 181 qkedagqyrcvankslgtavskvkvlefevaparlrapeshnvtfgsevtlhcctatgipy 240  
 QY 241 PTTWINGNNAVSSGTOESVKDRVIDSRLOLFTKPGLYTCTATNKHGEKSTAKAAT 300  
 Db 241 pttwingnnavssgtoesvkdrvidsrloqlftkpglytctatnkhgekstakaaat 300  
 QY 301 ISIAEWSKPOKDNKGCAYQYRGEVCNAYL-----AKDALVEL-NTSYADPEEAQELLVHT 354  
 Db 301 isiaewskpdknkgcayqyrge---gvlmgpgqekmlvflptshrdpedaqellvht 357  
 QY 355 AMNELKAVVSPYCPRAAALLCNHIFQECSPGVPTPIPICREYCLAVKELFCAKEWLME 414  
 Db 355 amnelkavvspycpraallcnhifqecspgvptpiPICREYCLAVKELFCAKEWame 417  
 QY 415 EKTIRGLYRSEMHLSVPKCSKLPSMHMDPTACARLPHLDYKNENLTFPMTSSKPSVD 474  
 Db 415 ektrglrseemhlsvpkcsklpsmhmdptacarlphldyknenkltfpmTSSKPSVD 469  
 QY 475 IPNLPSSSSSFSVPYISMVITISIMSSFAIFVLFTTLYCCRRKQMKKRESAAV 534  
 Db 475 ipnlp-astsfavspaysmtvsiivsalafaltivllyccrrkewknkreslav 528  
 QY 535 TLTLPSELLDRLHPNPMYORMPLLNPKLISLEYPRNNIEYVDIGEGAFGRVQARA 594  
 Db 535 tltlpselldrllhpnpmymrmpllnPKLISleyprnnieyrdigegafgrvfqara 588  
 QY 595 PGLLPYEPFTWAVAVKMLEASADMDQADFOREALMAEFNDPNIVKLLGVCAVGKPMCLL 654  
 Db 595 pgllypepftwvavkmlkeasadmgaqdfgreaalmaefndpnivkllyvcavgkpmcll 648  
 QY 655 FEYMAVGLNLEFLSMSPHTVCSLSHSDLSMRAOVSSPSPPLSCABOLCIAROVAAAGMA 714  
 Db 655 feymavglneflsmshpvtcsllshsdlsMRAOVSSpplscabqlciarqvaagma 708  
 QY 715 YISERKEFVHRDLATFNCLVGENMVKIADFGLSRNIVSADYYKANENDALPIRMMPESI 774  
 Db 715 yiserkefhrdlatfnclvgenmvkiadfglsrniysadykannendalpirmmpesi 768  
 QY 775 FYNRYTSDWAVAGVVLMEIFSYGLQPYYGMAHEVYYVRDGNILSCPENCPVELYNL 834  
 Db 775 fynrytseDwavgvvlmeifsyglqpyygmaheevlyvrDgnilscpenCpvelynl 828  
 QY 835 MRLCMSKLPADRPSTSIHRILERMCERAREGT 866  
 Db 835 mrlcmsklpadrpsfcsihrlilqrmceraregt 860

Search completed: August 16, 2002, 13:37:49  
 Job time: 109 sec

CC method uses a mutated pTKR nucleic acid which comprises a modification to the intracellular and extracellular domains, or comprises a modification to the intracellular domain and excludes any nerve growth factor receptor(s) (NGFR). The method uses mutated pTKR as a cell surface marker, and is useful for identifying genetically modified cells, especially immunoselection of transduced mammalian cells, and for identifying mammalian cells expressing a protein of interest. The genetically modified marked cells may be used in an autologous or allogeneic setting e.g. gene therapy for bone marrow transplants, graft facilitation or immune reconstitution.

CC Sequence 869 AA:

Query Match 100.0%; Score 4569; DB 22; Length 869;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 869; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRELVINPLVHILTVAFSGTEKLPKAPVITPLETVDAIVEATFMCAVESYPOEIS 60  
1 mrelvinplvhlitlvafsgtekpkapviltpletdaiveeatfmcavesypoeis 60  
61 WTRNKILIKLFDTRYISIRENGQLTILSVESDDGIYCCCTANNVGAVESGALQVKKM 120  
61 wtrnkililkfdtryisirengqltillsvedsdgiyccctannvgavescgalqvkmk 120  
121 PKTRPPINKKIIEGLKVLPCCTMGNPKPSVSWKNSDPLRENSRIAVESGSLRHNV 180  
121 pktrppinkkiieglkvlpctmgnpkpsvswknsdplrensrilavescslrhnv 180  
181 OKEDAGQYCVANSGTASVYKLEFEVFARILRAPESHNTFGSFTVLHCTATIPV 240  
181 okedagqyctvanstgatsvyklefevfarylrapeshntfgsftvlhctatipv 240  
241 PITWTEGNAVSSGSIQESVKRIDSRLQPLTRPGTLCTATNNGEKFSRAKAAT 300  
241 pitwtegnavssgsiqesvkridsrlqpltrpgtlctatnngekfstakaaat 300  
301 ISIAEMSKPOKDKNGYCAQYRGECVNAVAKDALVFLNTSYADPEEQELLVTANNEIK 360  
301 isiaemskpokdkngycayrgecvnavakdalvflntsyadpeeellvtanneik 360  
361 VVSPVCRPAEALCHNITFOECSPPGVPTPTICREYCAVAKELFCAKELVNEEKTHRG 420  
361 vvspvcrpaeealchnitfoecspgvptpticreycavakelfcakelvneekthrg 420  
421 LVRSEHMLISVPCSLPSMHWDPACARPHLDNKKENKTPTMTSSKSPVDIPNLS 480  
421 lyresehmllisvpcslpsmhwdpacarp hldnkkenktptmtsskspsvdiplnls 480  
481 SSSSSFSVSPITSMYIISIMSFALVLTITLVCCRRKONKKKKRSAAVTLTTP 540  
481 ssssfsvspitismyisimsfalfvltitlvccrrkonkkkkrsaaavtlttpp 540  
541 SELLDLRLHPNMYQMPPLLNKFLISLEYRNNIETVNDIGGAFGRVQARAPILPY 600  
541 selldlrlhpnmyqmppllnkflisleeyrnrietvndiggafgrvqarapilpy 600  
601 BEPTWAVAKLKEEAGADQADFOREAAALMAEPDNPYIKLLGVCAVGRMCLFEYMAI 660  
601 bep twavaklle e agadqadfo reaaalmaepdnp yikllgvca vgrmcl feymai 660  
661 GDLINEFLKMSPHYVCSLSHSDLSMRAQVSSPPPLSCAEOLCIRQVAGAYISEBK 720  
661 gdlineflkmsphyvcslishsdls mraqvsspppl scaeolcirqv agayisebk 720  
721 FVHDLATRNCLVGENMVKIADFGLSRNITYSADYYKANENDAIPIRMAPPESIFNRYT 780  
721 fvhdlatrnclvgenmvkiadfglsrni tysadyykanendaipirmappesifnryt 780  
781 TESDVMAAGVLTMEFSTGLQRYGMAHEEVYIYVADGILISCPENCPEVELYNMFLCMS 840  
781 tesdvmaagvltmefstglqrygmaheevyiyvadgiliscpenpevelynmflcms 840  
841 WTRNKILIKLFDTRYISIRENGQLTILSVESDDGIYCCCTANNVGAVESGALQVKKM 120  
841 wtrnkililkfdtryisirengqltillsvedsdgiyccctannvgavescgalqvkmk 120

841 KLPADRPSTIRHILERMCEBAGTYSV 869  
841 klpadrpstirhilmcebagtysv 869

RESULT 3  
ID AAW26611  
AAW26611 standard; protein; 869 AA.

AC AAW26611;

DT 27-JAN-1998. (first entry)

DE Human muscle-specific kinase (MUSK).

KW Receptor tyrosine kinase; muscle specific kinase; MUSK; Dmk; human ligand; agrin; diagnosis; therapy.

OS Homo sapiens.

PN MO9721811-72.

PD 19-JUN-1997.

PF 13-DEC-1996; 96MO-US20696.

PR 10-MAY-1996; 96US-0644271.

PK 15-DEC-1995; 95US-0008657.

PA (REG-) REGENERON PHARM INC.

PI Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD;

DR WPI; 1997-332783/30.

NR N-PSDB; AAT90473.

PT Nucleotide sequences encoding human agrin and muscle specific kinase and related receptor - used in diagnosis and treatment of disorder with muscle atrophy

PS Example 4; Fig 4; 120pp; English.

CC This polypeptide comprise a novel human receptor tyrosine kinase designated muscle specific kinase (MUSK) that is expressed in normal and denervated muscle. MUSK is alternatively referred to Dmk for denervated muscle kinase. The amino acid sequence was deduced from an isolated cDNA clone (see AAT90471). Rat MUSK (see CC AAW26610) has also been identified. Use of MUSK to generate anti-MUSK antibodies and in the diagnosis of neurological or other disorders is disclosed. Assay systems that may be used to detect and/or measure ligands that bind the musk gene product are provided. A claimed method of promoting the growth, differentiation or survival of MUSK receptor-expressing cells involves administration to the cell of agrin (see AAW26609). Such cells include muscle, heart, spleen, ovary and retina cells, or cells genetically engineered to express the MUSK receptor.

CC Sequence 869 AA:

Query Match 99.8%; Score 4558; DB 18; Length 869;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MRELVINPLVHILTVAFSGTEKLPKAPVITPLETVDAIVEATFMCAVESYPOEIS 60  
1 mrelvinplvhlitlvafsgtekpkapviltpletdaiveeatfmcavesypoeis 60  
61 WTRNKILIKLFDTRYISIRENGQLTILSVESDDGIYCCCTANNVGAVESGALQVKKM 120  
61 wtrnkililkfdtryisirengqltillsvedsdgiyccctannvgavescgalqvkmk 120





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QY 121 PKTRPPINVKIIIEGLKAVLPCTMGNPKPSVSWIKGDSPLKNSHIAVLESGSLRIHNV 180
DB 121 PKTRPPINVKIIIEGLKAVLPCTMGNPKPSVSWIKGDSPLKNSHIAVLESGSLRIHNV 180
QY 181 OKEDAGORCAVKNKSLGTAYSKVVKLEFEVFAIRILRAPESHNVTCSTYTLHCTATGIPV 240
DB 181 OKEDAGORCAVKNKSLGTAYSKVVKLEFEVFAIRILRAPESHNVTCSTYTLHCTATGIPV 240
QY 241 PTTWIENGNAVSSGSIQESVDRVIDSRLOLFTFKPGYTCIATNKGKSTAKAAT 300
DB 241 PTTWIENGNAVSSGSIQESVDRVIDSRLOLFTFKPGYTCIATNKGKSTAKAAT 300
QY 301 ISIAEKSPQDKNGCYCAQYRGECNNAVIAKDALVFLNTSYADPEAOELVHTANNEIK 360
DB 301 ISIAEKSPQDKNGCYCAQYRGECNNAVIAKDALVFLNTSYADPEAOELVHTANNEIK 360
QY 361 VVSPICRPAEALICNHIIFQECSPGVVPTPICREYCLAVKELCAKEMLVMEKTHRG 420
DB 361 VVSPICRPAEALICNHIIFQECSPGVVPTPICREYCLAVKELCAKEMLVMEKTHRG 420
QY 421 LYSEEMHLLSVKCSKLPKSMHMDPTACARLPHLIDYKNENLTFPPMTSSKPSVDIPNLPS 480
DB 421 LYSEEMHLLSVKCSKLPKSMHMDPTACARLPHLIDYKNENLTFPPMTSSKPSVDIPNLPS 480
QY 481 SSSSEFSPTYSMTVTIISISSPFIPLTLITTTTCCRRKKOMKKKRESAAVTLTLP 540
DB 481 SSSSEFSPTYSMTVTIISISSPFIPLTLITTTTCCRRKKOMKKKRESAAVTLTLP 540
QY 541 SELLDLRHPNMYORMLPLNPKLLSLEYERNNEIYRDIGEGAFGVFOBARAGILPY 600
DB 541 SELLDLRHPNMYORMLPLNPKLLSLEYERNNEIYRDIGEGAFGVFOBARAGILPY 600
QY 601 EPPFVNAVVKMLKEKESADMDQDFOREALMAEDPNPITVILLGVCAVGKPMCLLEFVAY 660
DB 601 EPPFVNAVVKMLKEKESADMDQDFOREALMAEDPNPITVILLGVCAVGKPMCLLEFVAY 660
QY 661 GDLNEPFRSMSPHTVCSHSDLSMRQVSSPGRPPSCACOLITARGVAGMAVLESEK 720
DB 661 GDLNEPFRSMSPHTVCSHSDLSMRQVSSPGRPPSCACOLITARGVAGMAVLESEK 720
QY 721 FVHRDLATRNCLVGENNVKIADEGLSRNIYSADYKANENDAIPIRMPESTIFYNRYT 780
DB 721 FVHRDLATRNCLVGENNVKIADEGLSRNIYSADYKANENDAIPIRMPESTIFYNRYT 780
QY 781 TESVNAVYGVVLMETFSYGLQPYTGMAHEVITYVRDGNILSCENCPVELYNMLCWS 840
DB 781 TESVNAVYGVVLMETFSYGLQPYTGMAHEVITYVRDGNILSCENCPVELYNMLCWS 840
QY 841 KLPADRPSTSIHRIERMCERAGTVSV 869
DB 841 KLPADRPSTSIHRIERMCERAGTVSV 869
QY 869 KLPADRPSTSIHRIERMCERAGTVSV 869
DB 869 KLPADRPSTSIHRIERMCERAGTVSV 869

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RESULT 4  
AAW26506 standard; Protein; 869 AA.  
AAW26506:  
06-JAN-1998 (first entry)  
Human Dmk receptor.  
Dmk receptor: tyrosine kinase receptor; signal transduction; assay;  
therapy; diagnosis; Alzheimer's disease; Parkinson's disease;  
amyotrophic lateral sclerosis; Lou Gehrig's disease;  
idiopathic torsion dystonia; muscle atrophy.  
Homo sapiens.  
US5656473-A.  
12-ADG-1997.

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XX 21-JUL-1993; 93US-0095658.
PF 19-JAN-1995; 95US-0374834.
PR 21-JUL-1993; 93US-0095658.
XX (REG- ) REGENERON PHARM INC.
PI Rojas EA, Valenzuela DM;
PI NPI; 1997-414593/38.
DR N-PSDB; AAT87073.
XX New isolated human denervated muscle kinase receptor - used to
PT develop products for the diagnosis and treatment of neurological,
PT muscle or neuromuscular disorders
XX Claim 4; Column 31-36; 31pp; English.
XX This polypeptide comprises the human Dmk receptor (AAW26506), a novel
CC tyrosine kinase receptor that is expressed in high levels in
CC denervated muscle. Its amino acid sequence was deduced from an
CC isolated nucleic acid molecule (see AAT87073). The Dmk receptor can
CC be used to screen for agents that interact with Dmk. Agents that
CC bind to the receptor may mediate survival and differentiation in
CC cells naturally expressing the receptor, but may also confer survival
CC and proliferation when used to treat cells engineered to express the
CC receptor. Dmk receptor polypeptides and polynucleotides can also be
CC used for detecting aberrancies in the function or expression of the
CC receptor which may be used in the diagnosis of muscular or other
CC disorders. Manipulation of the receptor or agonists which bind this
CC receptor may be used to treat neurological diseases, diseases of
CC muscle or neuromuscular unit disorders, including Alzheimer's
CC disease, Parkinson's disease, amyotrophic lateral sclerosis (Lou
CC Gehrig's disease), idiopathic torsion dystonia and muscle atrophy.
CC The extracellular domain (ECD) of the receptor can be used to block
CC the binding of receptor to target cells. A receptorbody comprising
CC the ECD fused to a human Ig gamma-1 constant region is claimed.
XX Sequence 869 AA:
SO
Query Match 99.8%; Score 4558; DB 18; Length 869;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MRELVIPIVHILITFAFGTEKLPKAPVITTPLEVDALVEVAFKCAVESEYPOEIS 60
DB 1 MELVPIPIVHILITVAISGTEKLPKAPVITTPLEVDALVEVAFKCAVESEYPOEIS 60
QY 61 WFNKILIKLFDTRYSIRENGOLITLSEDSDDGIYCTTANNVGAVESGALQVKM 120
DB 61 WFNKILIKLFDTRYSIRENGOLITLSEDSDDGIYCTTANNVGAVESGALQVKM 120
QY 121 PKTRPPINVKIIIEGLKAVLPCTMGNPKPSVSWIKGDSPLKNSHIAVLESGSLRIHNV 180
DB 121 PKTRPPINVKIIIEGLKAVLPCTMGNPKPSVSWIKGDSPLKNSHIAVLESGSLRIHNV 180
QY 181 OKEDAGORCAVKNKSLGTAYSKVVKLEFEVFAIRILRAPESHNVTCSTYTLHCTATGIPV 240
DB 181 OKEDAGORCAVKNKSLGTAYSKVVKLEFEVFAIRILRAPESHNVTCSTYTLHCTATGIPV 240
QY 241 PTTWIENGNAVSSGSIQESVDRVIDSRLOLFTFKPGYTCIATNKGKSTAKAAT 300
DB 241 PTTWIENGNAVSSGSIQESVDRVIDSRLOLFTFKPGYTCIATNKGKSTAKAAT 300
QY 301 ISIAEKSPQDKNGCYCAQYRGECNNAVIAKDALVFLNTSYADPEAOELVHTANNEIK 360
DB 301 ISIAEKSPQDKNGCYCAQYRGECNNAVIAKDALVFLNTSYADPEAOELVHTANNEIK 360
QY 361 VVSPICRPAEALICNHIIFQECSPGVVPTPICREYCLAVKELCAKEMLVMEKTHRG 420
DB 361 VVSPICRPAEALICNHIIFQECSPGVVPTPICREYCLAVKELCAKEMLVMEKTHRG 420

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OY 421 LYRSEHLLSVKCKSLPSMNDPACARLPHLDYKNENKTEPMTSSKPSVDIPNLS 480
DB 421 LYRSEHLLSVKCKSLPSMNDPACARLPHLDYKNENKTEPMTSSKPSVDIPNLS 480
OY 481 SSSSSFSVPTYSMTVITISIMSFALFVLTITLCCRRKKOKNKKRESAAVTLTLP 540
DB 481 SSSSSFSVPTYSMTVITISIMSFALFVLTITLCCRRKKOKNKKRESAAVTLTLP 540
OY 541 SELLDLRLHPNMQPMLLPKLLSLEYPRNNIEYVRDISEGAFGRVQARAPGLLP 600
DB 541 SELLDLRLHPNMQPMLLPKLLSLEYPRNNIEYVRDISEGAFGRVQARAPGLLP 600
OY 601 EPTTNAVAVKMLKEEASADMDQADPQREAAALAEFDPNPIVLLGVCAVGKPPCLLFEYMAX 660
DB 601 EPTTNAVAVKMLKEEASADMDQADPQREAAALAEFDPNPIVLLGVCAVGKPPCLLFEYMAX 660
OY 661 GDLNELRKSPPRTVCSLSHSDLSMRAOVSSPPPPPLSCAEOLCIAQVAAGAAYSERK 720
DB 661 GDLNELRKSPPRTVCSLSHSDLSMRAOVSSPPPPPLSCAEOLCIAQVAAGAAYSERK 720
OY 721 FVHRDLATRNCLGEMNVVYIADFGLSRNTYSADYKANEADAIPTRMPPEISIFYNRYT 780
DB 721 FVHRDLATRNCLGEMNVVYIADFGLSRNTYSADYKANEADAIPTRMPPEISIFYNRYT 780
OY 781 TESDVAVGVVLMIEFSYGIQPYGMAHEVIYVRDGNILSPENCPEVILMLRCLWS 840
DB 781 TESDVAVGVVLMIEFSYGIQPYGMAHEVIYVRDGNILSPENCPEVILMLRCLWS 840
OY 841 KLPADRPSTSHRILERNKCEAECTVSV 869
DB 841 KLPADRPSTSHRILERNKCEAECTVSV 869

RESULT 5
ID AAM26610 standard; Protein: 868 AA.
AC AAM26610;
DE 27-JAN-1998 (first entry)
XX Rat muscle-specific kinase (MUSK).
XX Receptor tyrosine kinase; muscle specific kinase; Musk; Dmk; rat;
XX ligand; agrin; diagnosis; therapy.
XX Rattus sp.
XX Key Location/Qualifiers
XX Peptide 1..19
XX Domain 21..492 /label- Sig_peptide
XX Domain 493..521 /label- Extracellular_domain
XX Domain /label- Transmembrane_domain
XX Domain 522..868 /label- Intracellular_domain

MO9721811-A2.
PD 19-JUN-1997.
PF 13-DEC-1996; 96WC-0520696.
PR 10-MAY-1996; 96US-0644271.
PR 15-DEC-1995; 95US-0008657.
XX (REGG-) REGENERON PHARM INC.
XX Bowen DC, Glaes DJ, Valenzuela DM, Yancopoulos GD:
PI WPI; 1997-332783/30.

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DR N-PSDB; AAT90472.
XX Nucleotide sequences encoding human agrin and muscle specific kinase
PT and related receptor - used in diagnosis and treatment of disorder
PT with muscle atrophy
XX Example 1; Fig 1; 120pp; English.
XX This polypeptide comprise a novel rat receptor tyrosine kinase
CC designated muscle specific kinase (Musk) that is expressed in
CC normal and denervated muscle. Musk is alternatively referred to
CC Dmk for denervated muscle kinase. The amino acid sequence was
CC deduced from an isolated cDNA clone (see AAT90472). Human Musk (see
CC AAM26611) has also been identified. Use of Musk to generate anti-
CC Musk antibodies and in the diagnosis of neurological or other
CC disorders is disclosed. Assay systems that may be used to detect
CC and/or measure ligands that bind the musk gene product are provided.
CC A claimed method of promoting the growth, differentiation or
CC survival of Musk receptor-expressing cells involves administration
CC to the cell of agrin (see AAM26609). Such cells include muscle,
CC heart, spleen, ovary and retina cells, or cells genetically
CC engineered to express the Musk receptor.
XX Sequence 868 AA:

Query Match 93.9%; Score 4292.5; DB 18; Length 868;
Best Local Similarity 93.2%; Pred. No. 0;
Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

OY 1 MRELNIPLVHLITLVAFSGTEKLPKAVITPTETVALVEVATPMCAVESYQPEIS 60
DB 1 mrelnplvgmltlvalsgteklpkavltptetvalveevatpmcavesypqels 60
OY 61 WTRNKILKLPDRTYSIRENQQLTILSVEDSDGIYCTANNGAVESGALQVWK 120
DB 61 wtrnkilkldrtysirengqltlilsvedsdgiyctannavgavesgalqvwmk 120
OY 121 PKTRPPINVKIIEGKAVLPCTMGNPKPSVWIKGSPLENSRIAVLESGLRIHV 180
DB 121 pktrppinvkiliegkavlpctmgnpkpsvwlkgsplesrriavlesgslrhv 180
OY 181 OKEDAGQRCVAKNSLSTAVSKVVKLEFEVPAIRPESNNVTFGSPVTLACRATGPV 240
DB 181 okedagqrcvaknslstavskvkvklefevparlpesnnvtfgspvltlcratgtpv 240
OY 241 PTIWIENGNAVSSGSIQESYKRVDSRLQLTTRKGLTYTCIATNKGKSTAKAAT 300
DB 241 ptwiengnavssgsiqesykrvdsrlqlttrkgltytciatnkgkstakaat 300
OY 301 ISLWNSKPKDNKGCAQYRGECNVLAKDALVFINTSYADBEAOELLVTRANMLK 360
DB 301 islwnskpkdnkgcaqyrgecnvlakdalvfintsyadbeaellvtranelk 360
OY 361 VSPVCRPAEALICNHFQECSPGVVPTPIPCREYLAVKELFCAKEMLVMEKTHRG 420
DB 361 vspvcrpaecalicnhfqecspgvvptpircreylavkelcfaemlvmekthrg 420
OY 421 LYRSEHLLSVKCKSLPSMNDPACARLPHLDYKNENKTEPMTSSKPSVDIPNLS 480
DB 421 LYRSEHLLSVKCKSLPSMNDPACARLPHLDYKNENKTEPMTSSKPSVDIPNLS 480
OY 481 SSSSSFSVPTYSMTVITISIMSFALFVLTITLCCRRKKOKNKKRESAAVTLTLP 540
DB 481 SSSSSFSVPTYSMTVITISIMSFALFVLTITLCCRRKKOKNKKRESAAVTLTLP 540
OY 541 SELLDLRLHPNMQPMLLPKLLSLEYPRNNIEYVRDISEGAFGRVQARAPGLLP 600
DB 541 SELLDLRLHPNMQPMLLPKLLSLEYPRNNIEYVRDISEGAFGRVQARAPGLLP 600
OY 601 EPTTNAVAVKMLKEEASADMDQADPQREAAALAEFDPNPIVLLGVCAVGKPPCLLFEYMAX 660
DB 601 EPTTNAVAVKMLKEEASADMDQADPQREAAALAEFDPNPIVLLGVCAVGKPPCLLFEYMAX 660

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QY 661 GDLEFLRSMSPHTVCSLSHSDLSMRAOVSSPPPLSCAEOCLCARQVAAAGMAYLSERK 720  
 DB 660 gdlneflrsmshphtvcslshtsdlsrarsvssppplscaeqlclarqvaagmaylsesrk 719  
 QY 721 FVHRDLATRNCLVGENMVKIADFGLSRNITSDYKANKENDAPIRMPPESTIFYNRYT 780  
 DB 720 fvhrlatrnclvgenmvkiadfglsrnltsadykagndaipirmppesitfynryt 779  
 QY 781 TESDVMAVGVLWMEIFSYGLOPYGMAHEVYIYVADGNILSCENCPVELYNLRCLWS 840  
 DB 780 tesdvavgvvlwmeifsyglopygmaheeviyvrdgnllacpencpvelynlmlrclws 839  
 QY 841 KLPRDRPSFTSIHRIELRMCEAECTVSV 869  
 DB 840 klprdrpsfcsihrlgrmceraegctvgv 868

RESULT 6

AAW26507 standard; Protein; 868 AA.

AAW26507;

06-JAN-1998 (first entry)

Rat Dmk receptor.

Dmk receptor; tyrosine kinase receptor; signal transduction; assay; therapy; diagnosis.

Rattus sp.

Location/Qualifiers  
 1..19  
 /label= Sig-peptide  
 Domain  
 20..492  
 /label= Extracellular  
 Domain  
 492..521  
 /label= Transmembrane  
 522..868  
 /label= Intracellular

US5656473-A.

12-AUG-1997.

21-JUL-1993; 93US-0095658.

19-JAN-1995; 95US-0374834.

21-JUL-1993; 93US-0095658.

(REG- ) REGENERON PHARM INC.

Rojas EA, Valenzuela DM;

WPI; 1997-414593/38.

N-PSDB; AAT87074.

New isolated human denervated muscle kinase receptor - used to develop products for the diagnosis and treatment of neurological, muscle or neuromuscular disorders

Example 1; Column 19-24; 31pp; English.

This polypeptide sequence comprises the rat Dmk receptor, a novel tyrosine kinase receptor that is expressed at high levels in denervated muscle. Its amino acid sequence was deduced from an isolated cDNA clone (see AAT87074). Human Dmk receptor (see AAW26506) has also been identified and can be used to develop products for the diagnosis and treatment of neurological, muscle or neuromuscular disorders.

SQ Sequence 868 AA;

Query Match

Best Local Similarity 93.9%; Score 4292.5; DB 18; Length 868;

Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

QY 1 MRELINPIVHILTLVAFSGTEKLPKAPVITTPLETVDALVEEATPMCAVESYPOPEIS 60  
 DB 1 mrelinpihlqmtlivafigsteklpkavpittpletvdalveeatpmcavesyppeis 60  
 QY 61 WTRNKILIKLFDRYSIRENGOLITLVEDSDGTCCTANNGVAGVASCALQYKMK 120  
 DB 61 wtrnkiliklfdrysirengqlitlsvedsdggtyccctannvgvagscgalqykmk 120  
 QY 121 PKITRPPINKIIEGLKAVLPCTTMGNPKPSVMIKDPSPLRENSRAVLESGLRIHNV 180  
 DB 121 pkitrppinkiliegkavlpcttmgnpkpsvmlkdsalrenslavlesgslrhnv 180  
 QY 181 QKEDAGYRCVANKSLGTAYSKVYLEFEVFARILAPESHNVTFSSFTLHCTANGIPV 240  
 DB 181 qkedagqrcvankslgtayskvylefevfarylapeseshnvtfssfvtlctangipv 240  
 QY 241 PTTWTIENGNAVSSGSIQSVKDRVIDSRLOLEITKPGLYTCTATKRGKSTAKAAT 300  
 DB 241 pttwtiengnavssgsiqsvkdrvidsrldleltkpglytctatknkhekstakaaat 300  
 QY 301 ISTAEKSKQKKNKGCACQYRGECVNAVLAQDALVELNTSYADPEBAQELVTTANNEK 360  
 DB 301 istaekskqkknkgcacqyrgecvnavlqadalelntsyadpebaqelvttannek 360  
 QY 361 VVSPVCRPAEALLCNHRIOECSPGVPPPIPCREYCAVVEIPCAKMLVKEETHNG 420  
 DB 361 vvspvcrpaalclcnhrioecspgvpppircreycavveipcakmlvkeethng 420  
 QY 421 KYRSEMHLSVPCSKSLSMHMDPTFACARLPHLDYKNENLKFPPMTSSKPSVDIPNLS 480  
 DB 421 kyrselmhlsvpcskslsmhmdptfacarlphldyknenlkfppmtsskpsvdipnls 480  
 QY 481 SSSSFSVSPRTSMVTIISIMSSFAIFVLITTTIXCCRRRQKKNKRESAAVTLTTP 540  
 DB 481 ssssfsvsprrtsmtvtiisimssfaifvlitttixccrrrqqkknkresaaavtlttp 540  
 QY 540 astsfavspysmtvtiisimscfavliltltyccrrrremkkrresaavtlttp 539  
 QY 541 SELLDRLHPNMQRMELLPKLLSLDEPRNNIEYVRDIEGAFGRVFOARAGLLPY 600  
 DB 540 sellldrlhpnmqrmellpkllsldeprnnieyvrddiegafgrvfoaragllpy 600  
 QY 601 EPFTVAAYKMLKEASADMOADFOREALMAEFDPNIVKLLGVCAVGRPKCLTEFNAY 660  
 DB 600 eptmvaaykmlkeasadmqadfgreaalmaefdpnivkllgvcavgkpmcllfeymay 659  
 QY 661 GDLEFLRSMSPHTVCSLSHSDLSMRAOVSSPPPLSCAEOCLCARQVAAAGMAYLSERK 720  
 DB 660 gdlneflrsmshphtvcslshtsdlsrarsvssppplscaeqlclarqvaagmaylsesrk 719  
 QY 721 FVHRDLATRNCLVGENMVKIADFGLSRNITSDYKANKENDAPIRMPPESTIFYNRYT 780  
 DB 720 fvhrlatrnclvgenmvkiadfglsrnltsadykagndaipirmppesitfynryt 779  
 QY 781 TESDVMAVGVLWMEIFSYGLOPYGMAHEVYIYVADGNILSCENCPVELYNLRCLWS 840  
 DB 780 tesdvavgvvlwmeifsyglopygmaheeviyvrdgnllacpencpvelynlmlrclws 839  
 QY 841 KLPRDRPSFTSIHRIELRMCEAECTVSV 869  
 DB 840 klprdrpsfcsihrlgrmceraegctvgv 868

RESULT 7

AAW26507 standard; Protein; 868 AA.

AAW26507;



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 16, 2002, 13:36:00 ; Search time 15.06 Seconds

(without alignment)  
2334.216 Million cell updates/sec

Title: US-09-817-487a-2

Perfect score: 4569

Sequence: 1 MRELVNIPVLVILTVAFSG.....TSIHRIILRCMCEAGCTVSV 869

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	906.5	19.8	937	1	ROR1_MOUSE
2	899	19.7	937	1	ROR1_HUMAN
3	886.5	19.4	944	1	ROR2_MOUSE
4	876	19.2	943	1	ROR2_HUMAN
5	862	18.9	821	1	TRKB_MOUSE
6	861	18.8	822	1	TRKB_HUMAN
7	858	18.8	818	1	TRKB_MOUSE
8	854.5	18.7	1051	1	TRKB_RAT
9	833	18.2	1051	1	PRK7_CHICK
10	813	17.8	827	1	TRKC_CHICK
11	812	17.8	796	1	TRKA_HUMAN
12	792.5	17.3	835	1	TRKC_HUMAN
13	788.5	17.3	825	1	TRKC_PIG
14	781.5	17.1	799	1	TRKA_RAT
15	774	16.9	1070	1	PRK7_HUMAN
16	768	16.8	864	1	TRKC_RAT
17	751	16.4	778	1	TRKA_CHICK
18	706	15.5	806	1	CEK2_MOUSE
19	703.5	15.4	801	1	CEK3_MOUSE
20	702	15.4	823	1	CEK3_CHICK
21	701	15.3	806	1	FGR3_MOUSE
22	698.5	15.3	812	1	FGR3_HUMAN
23	693.5	15.2	802	1	FGR4_XENLA
24	683	14.9	821	1	FGR2_HUMAN
25	677	14.8	822	1	FGR1_HUMAN
26	677	14.8	880	1	TYO3_MOUSE
27	675.5	14.8	808	1	FGR4_MOUSE
28	675	14.8	819	1	FGR1_CHICK
29	675	14.8	822	1	FGR1_MOUSE
30	671.5	14.7	821	1	FGR2_MOUSE
31	669	14.6	822	1	FGR1_RAT
32	669	14.6	880	1	TYO3_RAT
33	667	14.6	1383	1	INSR_RAT

## ALIGNMENTS

```

RESULT 1
ID ROR1_MOUSE STANDARD: PRT: 937 AA.
AC Q9Z139,
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tyrosine-protein kinase transmembrane receptor ROR1 precursor
DE (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 1)
DE (MROR1).
GN ROR1 OR NTRKR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99248426; PubMed=10231392;
RA Oishi I., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T., Liu Z.,
RA Hattori T., Akita S., Matsuda Y., Yamamura H., Otsu H., Minami Y.;
RT "Spatio-temporally regulated expression of receptor tyrosine kinases,
RT mror1, mror2, during mouse development: implications in development
RT and function of the nervous system.";
RL Genes Cells 4:41-56(1999).
CC -1- FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR WHOSE ROLE IS NOT YET
CC CLEAR.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (Fz) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CC DOMAIN. BELONGS TO THE ROR SUBFAMILY.
CC -----
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CC -----
CC EMBL: AB010383; BAA75480.1; -.
CC HSSP: P00747; ICEA.
CC MGD: MGI:1347520; Ror1.
CC InterPro: IPR000719; Euk_Pkinase.
CC InterPro: IPR000024; Fz_domain.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003598; Ig_C2.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR001245; Tyr_Pkinase.
CC Pfam: PF01392; Fz; 1.
CC Pfam: PF00047; Ig; 1.
CC Pfam: PF00051; kringle; 1.
CC Pfam: PF00069; pkinase; 1.

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DR PRINTS; PRO0018; KRINGLE.
DR PRINTS; PRO0109; TYRKINASE.
DR SMART; SM00408; ICG2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00219; TYRKC; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS00021; KRINGLE_1; FALSE_NEG.
DR PROSITE; PS0070; KRINGLE_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR Transferrase; Tyrosine-protein kinase; ATP-binding; Receptor;
KW Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
KM Immunoglobulin domain.
FT SIGNAL 1 29
FT CHAIN 30 937
FT DOMAIN 30 406 POTENTIAL.
FT TRANSMEM 407 427 TYROSINE-PROTEIN KINASE TRANSMEMBRANE
FT DOMAIN 428 937 RECEPTOR RORL.
FT DOMAIN 773 139 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 165 299 POTENTIAL.
FT DOMAIN 312 391 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 473 746 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 753 782 F2.
FT DOMAIN 784 851 KRINGLE.
FT DOMAIN 853 876 PROTEIN KINASE.
FT N-BIND 479 487 SER/THR-RICH.
FT BINDING 506 506 ATP (BY SIMILARITY).
FT ACT_SITE 615 615 ATP (BY SIMILARITY).
FT MOD_RES 645 645 BY SIMILARITY.
FT DISULFID 79 131 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CARBOHYD 47 47 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 66 66 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 937 AA; 104156 MW; D728733E67D1782C CRC64;

Query Match 19.88; Score 906.5; DB 1; Length 937;
Best Local Similarity 29.66; Pred. NO. 4.4e-53;
Matches 241; Conservative 106; Mismatches 233; Indels 215; Gaps 24;

QY 123 ITRPPIVKKIIEGLKAVLPCTTGNPKPSVSWIKGDSPTRENSRI--AVLESGLSRH 178
DB 60 LDEPMNNTITSLGOTAEHLCHVSGNPPPSIKWFKNDAPVYGEPRISFRATNYSRLR 119
QY 179 NVQKEDAGQYRCVAKNSLGNVSKVVKLEFEVFAKILRAPESHAVTQSGEYTLHCTATGI 238
DB 120 NLDTTDTGTFQCVATNG-----KKVVSITGYLF-----VKFG----- 151
QY 239 PVPTITMENGNNAVSSGSIQESVDRVIDSLQFLITKPGLYCIATNKGKFSKAA 298
DB 152 PPTP-----ASPSSDEYED----- 167
QY 299 ATISIAEKSPQKDNKGCAQYRGEVCNAVLAQDALVFLNTSYDPE-EAQELLVHTAMN 357
DB 168 -----GFCOPYRGIAQ-ARFIGNRTVMESLIHQGELENDITAFATWIG 210
QY 358 ELKVVSPVCRPAEALLCNHIEFGQC-SFGVYPTPIPCREKCLAVKEFLCKEMLVMEK 416
DB 211 TSHSLDCKGQFAIPSLCHYAFPYCDETSYVKKPRDLCRDCEVLNVLCOTEYI----- 265
QY 417 THRGLYSE--MHLLSVKCSKSLPSMHMDPTA-CAR-LPHLDYKNENLTFP----- 464
DB 266 -----FARSNPILMRKLRKLPNCEDELPPQSPPEANCIIRIGIMADPINKNHKCYNSTGV 321
QY 465 -----PMTSKSPVDIPNL-----PSSSSS---FSVSTY 492
DB 322 RGTAVSVTKSGHOCQPMNSQYPHTHSFALRPELNGHSHYCRNPGNCKEAPWCFTLDENF 381
QY 493 -----SMTVIISMSFAIPVLLITLITLTYCCRRKKMKNNKRRSAA 533

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DB 382 KSDLCDIPACDSKDSKKNKMEILYILVPSVALPLAIAELFFEICVCRNNOKSS----- 435
QY 534 VLTITLPSSELLDRLPNMYORMP-----LLN---PKLSLEYPRNRIEYVD 580
DB 436 -----SPVQROPVPYGVQNVEMSLNAYRKKSAKELPLSAVFME 478
QY 581 ICGAGRYVFOAR--APGLLPYEPFTMAVVKMLKEBASADMDQFQREALAAEDNPNI 638
DB 479 LGECTGKIKYKGLYLPGM---DHAQLVAIKTLKDYNNPQOWTEFQOEASLMAELHHPI 535
QY 639 VLLGVCAVCKPMLCLPEYKAYADLNEFLRSMSPHVCVLSHSDLSMRQVSPGPPPS 698
DB 536 VCLLGAVTQDPYCMPEYVNOGDHLHFLMRSP-----HSDVCCSSDEDTYKSSSD 588
QY 699 CAEOLCIARQVAGMAVLSERKFFVHRDLATRCNLGEMNVYKTADEGLSRNITYSADYKA 758
DB 589 HGDFLHAIDIAAGMEYLSHFVHDLARNTLIGQLHVKISDGLSNEYISADYVR 648
QY 759 NENDAIPIRMPPESIFNRYRTESDVAVGVVLMETFGLOPYTGMAHEVIYVRG 818
DB 649 QSKSLPIRMPPPEALMYGKFSSDSIWSGVVLWETFSGLOPYYGFNSQEVIEVRRK 708
QY 819 NIISCPCVVELYNLMRLQMSKLPADPSESTH 853
DB 709 QLLPCEDECPRMYSILMTECWEIPSRPRKDIH 743

RESULT 2
RORL_HUMAN STANDARD; PRT; 937 AA.
ID RORL_HUMAN
AC 001973; 092776;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tyrosine-protein kinase transmembrane receptor ROR1 precursor
DE (BC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 1).
GN ROR1 OR NTRK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE=93100347; PubMed=1334494;
RA Maslakowski P., Carroll R.D.;
RT "A novel family of cell surface receptors with tyrosine kinase-like
RT domain.";
RL J. Biol. Chem. 267:26181-26190(1992).
RN [2]
RP SEQUENCE FROM N.A. (SHORT ISOFORM).
RX MEDLINE=97030043; PubMed=8875995;
RA Reddy U.R., Phatak S., Pleasure D.;
RT "Human neural tissues express a truncated Ror1 receptor tyrosine
RT kinase, lacking both extracellular and transmembrane domains.";
RL Oncogene 13:1555-1559(1996).
CC -1- FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR WHOSE ROLE IS NOT YET
CC CLEAR.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM/T-ROR1 ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED STRONGLY IN HUMAN HEART, LUNG, AND
CC KIDNEY, BUT WEAKLY IN THE CNS. THE SHORT ISOFORM IS STRONGLY
CC EXPRESSED IN FETAL AND ADULT CNS AND IN A VARIETY OF HUMAN
CC CANCERS, INCLUDING THOSE ORIGINATING FROM CNS OR PNS
CC NEUROECTODERM.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS DURING EARLY
CC EMBRYONIC DEVELOPMENT. THE EXPRESSION LEVELS DROP STRONGLY AROUND
CC DAY 16 AND THERE ARE ONLY VERY LOW LEVELS IN ADULT TISSUES.
CC -1- SIMILARITY: CONTAINS 1 FRITZLEED (F2) DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.

```



CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC  
 CC DOMAIN. BELONGS TO THE ROR SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@isb.ch](mailto:license@isb.ch)).  
 CC -----  
 DR EMBL: M97675; AAA60275.1; -;  
 DR EMBL: U38894; AAC50714.1; -;  
 DR HSSP: P00747; ICEA.  
 DR MIM: 602336; -;  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000024; Fz\_domain.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_C2.  
 DR InterPro: IPR000001; Kringle.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF01392; Fz; 1.  
 DR Pfam: PF00047; Kringle; 1.  
 DR Pfam: PF00051; Kringle; 1.  
 DR Pfam: PF00059; Kringle; 1.  
 DR PRINTS: PR00108; KRINGLE.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00408; IGC2; 1.  
 DR SMART: SM00130; KR; 1.  
 DR SMART: SM00219; TYRK; 1.  
 DR PROSITE: PS50038; F2; 1.  
 DR PROSITE: PS50021; KRINGLE\_1; FALSE\_NEG.  
 DR PROSITE: PS50070; KRINGLE\_2; 1.  
 DR PROSITE: PS50107; PROTEIN\_KINASE\_ATP; FALSE\_NEG.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS50109; PROTEIN\_KINASE\_TYR; 1.  
 DR Transmembrane: Tyrosine-protein kinase; ATP-binding; Receptor;  
 KM Transmembrane: Signal; Glycoprotein; Kringle; phosphorylation;  
 KM Immunoglobulin domain; Alternative splicing.  
 FT SIGNAL 1 29  
 FT CHAIN 30 937  
 FT DOMAIN 30 406  
 FT TRANSMEM 407 427  
 FT DOMAIN 428 937  
 FT DOMAIN 73 139  
 FT DOMAIN 165 299  
 FT DOMAIN 312 391  
 FT DOMAIN 473 746  
 FT DOMAIN 753 782  
 FT DOMAIN 784 851  
 FT DOMAIN 853 876  
 FT NP\_BIND 479 487  
 FT BINDING 506 506  
 FT ACT\_SITE 615 615  
 FT MOD\_RES 645 645  
 FT DISULFID 79 131  
 FT CARBOHYD 47 47  
 FT CARBOHYD 66 66  
 FT CARBOHYD 184 184  
 FT CARBOHYD 315 315  
 FT VARSPPLIC 549  
 FT SEQUENCE 937 AA: 104312 MW: 0D0694DBF296F4773 CRC64;

Query Match 19.7%; Score 899; DB 1; Length 937;  
 Best Local Similarity 31.5%; Pred. No. 1.4e-52;  
 Matches 229; Conservative 102; Mismatches 254; Indels 142; Gaps 20;

OY 221 HAVT--FGSFVTLHCTATGTPPTIWIENGNAVSGSIOESYKDRVIDSRQ---LFTT 275  
 Db 65 NNTTSLGOTAEHLCKVSGNPPTIWMFNDAVVOEPRRLSRSTIYGSRLRLRLDPT 124

OY 276 KPGLYTCTATNKHGEKSTAKAATISTAEMSKP-----QDNKGCAOYRGEVCAVLAK 331  
 Db 125 DTGYFOVATNGKEVYSTGLVFKFGPPPTASPGYSDEYDEDFCQPRSIAC-ARRIG 183  
 OY 332 DALVFNTSYADPE-EOAELLVHTAMNKLKVSPYCRPAEALCNHIFQEC-SGVAVPT 389  
 Db 184 NRTYVMSLHMOGELNENITAFIMIGISSHLSDKCSQFALPSLCHVAFPCDETSYVK 243  
 OY 390 PIPICREYCLAVKELFCAKKELVMEKTHRGLYNSE--MHLSVPKCSKLPMSHMDPTA 446  
 Db 244 PRDLRCDECELLENVLCOTEYI-----FARSNPMLRLKLPNCEDLPQESPEEA 294  
 OY 447 -CAR--LPHLIDNKENKTE-----PMTSSKPSV----- 473  
 Db 295 NCITIGIPMADPIKNKNCINSTGVDRGVSVTKSGRQCOPMNSQYPRHTFTALRPE 354  
 OY 474 -----LLIN---PKLISLEYPNNIEYVRDIEGAFGRYEQAR--APGLLPYEPTMV 606  
 Db 355 LINGHSYCRNPGNOKEAAPWCTLDENFKSDCLDIPACDSKSKRKN-----KMEILYIV 409  
 OY 502 SSFAIFVLLITTYCCRRRKKOMKKRESAAVTLTLPSELLDLRLHPNMQRMP-- 558  
 Db 410 PSVAIPPLAIALLEFFICVR---NNOKSSAPV-----OROPKHV 446  
 OY 559 -----LLIN---PKLISLEYPNNIEYVRDIEGAFGRYEQAR--APGLLPYEPTMV 606  
 Db 447 RGVAVEMSLNAYKPKAKAELPLSAVRMELESCAFGKTYKGLHYLPGR--DHAOLV 503  
 OY 607 AVKMLKEASADQADFOREALMAEFDPNPVYLLGCAVGVKPMCLLFEYMAVDNEF 666  
 Db 504 AIKTLKYNPQOMQMEFOQASLMAELHNPVCLLGAVQOEQVCLFEYINGDLEH 563  
 OY 667 LRSMPHTVCSLSDSMRAQVSSPPPLSCAEQICIRQVAAAGAYLSERFYARDL 726  
 Db 564 LIRSP-----HSDVCGSSDEDEGYTKSLDHGDFIHLAQLAGVEYSSHFVKDL 616  
 OY 727 ATRNCLVGENMYKIADFGLSRNTYSADYYKAMENDAPIRMPPEISIFYNRYTTESDV 786  
 Db 617 AARNILGLDHLKVISDLGLSREIYSADYRVQSKSLPIRMPPEALIMYKTSDDSDIN 676  
 OY 787 AYGVLMEISYGLQPYGYMAHEVITYYVDGNILSPENCPELYLMLRLCKSLPADR 846  
 Db 677 SFGVLMELTFSGLQPYGYFSGNOEIVEMVRKROLLPCSEDCPPMWSLMECWNELPSRR 736  
 OY 847 PSEFTSH 853  
 Db 737 PRFKDIH 743

RESULT 3  
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 ID ROR2\_MOUSE  
 AC 092138;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tyrosine-protein kinase transmembrane receptor ROR2 precursor  
 DE (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 2)  
 DE (ROR2).  
 GN ROR2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99248426; PubMed=10231392;  
 RA Oishi T., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T., Liu Z.J.,  
 RA Hata T., Akira S., Matsumura Y., Yamamura H., Otani H., Minami Y.,  
 RT Spatio-temporally regulated expression of receptor tyrosine kinases,  
 RT mror1, mror2, during mouse development: implications in development  
 and function of the nervous system.";  
 RL Genes Cells 4:41-56(1999).

Query Match	19.4%;	Score 866.5;	DB 1;	Length 944;
Best Local Similarity	28.3%;	Pred. No. 9,76-52;		
Matches 243;	Conservative 125;	Mismatches 257;	Indels 233;	Gaps 30;
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Db	93	VKMLKNDAPVYQPPRRVYIRKTEYGSRLRIQDLDITDGYGCVATNGTKT-----	143	
QY	208	FEVFARIILAPESHAVTGFSEVTLHCTATGIPVPIITMIENGNNAVSSGISDSVADRYID	267	
Db	144	-----ITATGV-----	149	
QY	268	SRLOFLTRKPGLYTCIA--TNKGEKFSPAKAAATISIAEMSKPKQDNK--GYCAQYREGV	324	
Db	150	-----LYVALGPHSPNHNF-----	181	
QY	335	CNAVIAKDALVFLNTSYADPEEAQ---ELVYTANNEKV---VSPVCRPAEALLCNII	378	
Db	182	CAREIGN-----RTIYVDSLQMOGEIERITIAAFTMTIGTSTOLDQCGQFAIPSCFCHV	235	
QY	379	POECSP-GVVPPTPIPCRECYCLAVELFCFAEMLVMEKTHGLYRSE---MHLLSVKPC	434	
Db	236	FPLCDACSAAPRPRELCRCCEVLENDLCROEYTLA-----RSNPLIMLRQLPKC	286	
QY	435	SKLPSEMDPTA--CARLP-----HLDYN-----KELUKTFP-----P	465	
Db	287	EALP--NPESPDANCMRIGIIPARLGRVHCQNGSGADRGMASTTKSGHCOQPALQHP	345	
QY	466	MSSKPSVDIPLN-----PSSSSSFYS-----SPTY---SMTYI	497	
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QY	498	ISIMSSFAI-FVLLITITLLYC--CRRRKQMKKKRESAAV---TLTPRSELLDRLEPN	551	
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QY	552	PMTQRPILLNKELSL--EYPRNNIEFYVDIEBGAQRFQOARAPSLYEPEFTVAYVM	610	
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QY	731	CLVGEVMVYKADIADFGISRNITADYKANKENDAIPIRMPMPESIFYNRYTTESDVAAQV	790	
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QY	791	VIMEIFSGLQPYGMAHEBYIYVDGNILSCPEMCAPVELYIUMLMCLSKLPADPPST	850	
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ID ROR2\_HUMAN STANDARD: PRT: 943 AA.  
 AC Q01974; Q9HAV7; Q9H6B1;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tyrosine-protein kinase transmembrane receptor ROR2 precursor  
 DE (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 2).  
 GN ROR2 OR NTRK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
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 RX MEDLINE=93100347; PubMed=1334494;  
 RA Maslakowski P., Carroll R.D.;  
 RT "A novel family of cell surface receptors with tyrosine kinase-like  
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 RL J. Biol. Chem. 267:26181-26190(1992).  
 RN (2)  
 RP SEQUENCE OF 34-943 FROM N.A., AND VARIANT ILE-819.  
 RX MEDLINE=20164326; PubMed=10700182;  
 RA Oldridge M., Fortuna A.M., Maringe M., Popping P., Mansour S.,  
 RA Pollitt C., Dechlara T.M., Kimble R.B., Valenzuela D.M.,  
 RA Yancopoulos G.D., Wilkie A.O.M.;  
 RT "Dominant mutations in ROR2, encoding an orphan receptor tyrosine  
 kinase, cause brachydactyly type B";  
 RL Nat. Genet. 24:275-278(2000).  
 RN (3)  
 RP SEQUENCE OF 34-574 FROM N.A., AND VARIANT THR-245.  
 RX MEDLINE=20442029; PubMed=10986040.  
 RA Schwabe G.C., Tinschert S., Buschow C., Melnick P., Wolff G.,  
 RA Gillissen-Kaesbach G., Oldridge M., Wilkie A.O.M., Koemec R.,  
 RA Mundlos S.;  
 RT "Distinct mutations in the receptor tyrosine kinase gene ROR2 cause  
 brachydactyly type B";  
 RL Am. J. Hum. Genet. 67:822-831(2000).  
 RN (4)  
 RP VARIANTS RRS C-184; W-189; W-366 AND K-620.  
 RX MEDLINE=20392394; PubMed=10932186;  
 RA Afzal A.R., Rajab A., Fenske C.D., Oldridge M., Elanko N.,  
 RA Terres-Pereira E., Tunesuez B., Murday V.A., Patton M.A.,  
 RA Wilkie A.O.M., Jeffery S.;  
 RT "Recessive Robinow syndrome, allelic to dominant brachydactyly type B,  
 is caused by mutation of ROR2";  
 RL Nat. Genet. 25:419-422(2000).  
 RN (5)  
 RP VARIANT RRS TYR-182.  
 RX MEDLINE=20392395; PubMed=10932187;  
 RA van Bokhoven H., Celli J., Kayserili H., van Beusekom E., Balci S.,  
 RA Brussel W., Skovby F., Kerr B., Percin E.F., Akarsu N., Brunner H.G.;  
 RT "Mutation of the gene encoding the ROR2 tyrosine kinase causes  
 autosomal recessive Robinow syndrome";  
 RL Nat. Genet. 25:423-426(2000).  
 RN (6)  
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 RA van Bokhoven H., Celli J., Kayserili H., van Beusekom E., Balci S.,  
 RA Brussel W., Skovby F., Kerr B., Percin E.F., Akarsu N., Brunner H.G.;  
 RL Nat. Genet. 26:383-383(2000).  
 CC -1- FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR WHICH MAY BE INVOLVED  
 IN THE EARLY FORMATION OF THE CHONDROCYTES. IT SEEMS TO BE  
 REQUIRED FOR CARTILAGE AND GROWTH PLATE DEVELOPMENT.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein  
 tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS DURING EARLY  
 EMBRYONIC DEVELOPMENT. THE EXPRESSION LEVELS DROP STRONGLY AROUND  
 DAY 16 AND THERE ARE ONLY VERY LOW LEVELS IN ADULT TISSUES.  
 CC -1- DISEASE: DEFECTS IN ROR2 ARE A CAUSE OF BRACHYDACTYLY TYPE B  
 (BDB). BDB IS AN AUTOSOMAL DOMINANT SKELETAL DISORDER  
 CHARACTERIZED BY HYPOPLASIA/APLASIA OF DISTAL PHALANGES AND NAILS.  
 IN BDB THE MIDDLE PHALANGES ARE SHORT BUT IN ADDITION THE TERMINAL  
 PHALANGES ARE RUDIMENTARY OR ABSENT. BOTH FINGERS AND TOES ARE

CC AFFECTED. THE THUMBS AND BIG TOES ARE USUALLY DEFORMED.  
 CC -1- DISEASE: DEFECTS IN ROR2 ARE A CAUSE OF RECESSIVE ROBINOW SYNDROME  
 (RRS). RRS IS AN AUTOSOMAL DISORDER CHARACTERIZED BY SKELETAL  
 DYSPLASIA WITH GENERALIZED LIMB BONE SHORTENING, SEGMENTAL DEFECTS  
 OF THE SPINE, BRACHYDACTYLY AND A DYSMORPHIC FACIAL APPEARANCE.  
 CC -1- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.  
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC  
 DOMAIN. BELONGS TO THE ROR SUBFAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC EMBL: AF28

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FT DOMAIN 473 746 PROTEIN KINASE.
FT THR 753 782 SER/THR-RICH.
FT DOMAIN 784 857 PRO-RICH.
FT DOMAIN 859 882 SER/THR-RICH.
FT NE_BIND 479 487 ATP (BY SIMILARITY).
FT BINDING 507 507 ATP (BY SIMILARITY).
FT ACT_SITE 615 615 BY SIMILARITY.
FT MOD_RES 646 646 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT DISULFID 83 135 BY SIMILARITY.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 318 318 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 182 182 C -> Y (IN RRS).
FT VARIANT 184 184 /FTID=VAR_010911.
FT VARIANT 189 189 R -> C (IN RRS).
FT VARIANT 189 189 /FTID=VAR_010768.
FT VARIANT 245 245 R -> W (IN RRS).
FT VARIANT 245 245 /FTID=VAR_010769.
FT VARIANT 366 366 A -> T.
FT VARIANT 366 366 /FTID=VAR_010912.
FT VARIANT 620 620 R -> W (IN RRS).
FT VARIANT 620 620 /FTID=VAR_010770.
FT VARIANT 819 819 N -> K (IN RRS).
FT VARIANT 819 819 /FTID=VAR_010771.
FT SEQUENCE 943 AA; 104726 MW; DBAC1E4622B5ECA0 CRC64;

Query Match 19.28; Score 876; DB 1; Length 943;
Best Local Similarity 28.68; Pred. No. 4.9e-51;
Matches 236; Conservative 119; Mismatches 249; Indels 222; Gaps 26;

OY 126 PPIVKKIEGKAVLPCTMGNPSPVSMIGKDSPLRENSRIAYL---ESGS-TRIHNWQ 181
DB 67 PVNNITVQGFALHCKVAGNPPNPNVWMLNDAPVQDEPRRIIRKREYSRLRIQDLD 126
OY 182 KEDAGQRCVAKNSLGTAVSKVVKLEFEVFAILRAPESHNVGTGSEVTLTCTATGIVP 241
DB 127 TTDGYGVQCVATNGMKT-----ITATGV--- 149
OY 242 TITMIENNNAVSSGSIQSVKDVDRIDSRLQLEITKPGIYTCIATNKKHGEKSTKAATI 301
DB 150 -----LTV----- 158
OY 302 SIAMSKPQDKNGKCYAQYRGEVGNNAVLAQDALVFLNTSVADPEBAQ---ELVHTAMNE 358
DB 159 SPNNHFODDYHEDGFCQYRGIAACARFIGN-----RTIYVDSIQMGEIENRITAAFTM 212
OY 359 LKV---VSPVCRPAAEALCNHIFQEC-SPGVVPPIPTICREYCLAVKELFCAKEMLYME 414
DB 213 IGTSTHLSDDQSOFAIPSECFHFVPLCDARAPRPRELCDECEVLESDLCROEYITA- 271
OY 415 EKHRTGLVRSF---MHLISVPCSKLPSMMDPTA---CARLP-----HLDVN--- 456
DB 272 -----KSNPLILMIQDLPKCEALP-MPESPDAANCMRIGIAPERLGRTHOCYNSGM 322
OY 457 -----KKNLKTFF-----PMTSKSPVDIPNL----- 478
DB 323 DYRGASTTKSGHQOQPMALQHPHSHTLSSTDFELGGAHYCNRPMGOMEGMFCFTQNK 382
OY 479 -----PSSSSSFVSFTYSMTVITISMSFAI-FULLITTLTYLC-CRRKKOMNKK 527
DB 383 NVRMELCDVPSCSPRDS-----KMGILYILVPSIAIPVLVLAICLFELVCMGR-----NK 431
OY 528 KRESAAV---TLTIPSELLDRNHRPMYQORPMLNPLPLSLD-EVRNNIEYVRDIG 582
DB 432 OKASASTPQRQLMASPSQDM-----EMPLINOHQAKIKELSLSVRFMEELG 480
OY 583 EGAGGVFOARAPGILPPEFTTNAVKMLKEASADQADQREDAALAEFDNPVIVLL 642
DB 481 EDRGKVKYKGLHFGPAREBOQVAVALIKTLKKAEGRLREERFNHEMLARQIHRVIVCLL 540

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OY 643 GVCAGKPMCLLFEPYMAAGDLINEFLRSKSPHTVCSLSHSDLSMRAOYSSPGPPPLSCAQ 702
DB 541 GVTAKDQPLSIFSYCSHGDLHEFLVMSRPSHSDVGTDDDTKVSALPEP-----DF 592
OY 703 LCIRQVAAAGKAVYSEKKEVYRDLATRCGLVGENMMYKIAIDFGSLRNISDYTKANEND 762
DB 593 VHLVAQIAAGAEVLSHHVARKDLATRVLYDKLANKISDGLFREYADADYKLLGNS 652
OY 763 AIPTRMPPEISIFPNRYTTESDVMAVGVLMEIFSYGLQPYGMAHEEVIYVRDGNILS 822
DB 653 LIPTRMAPEALIMGKRSIDSDISYGVLMVEVSYGLQPYCGYSNDVYMINRQVLP 712
OY 823 CPENCPELVNLMRLCWSKLPADRPSTSHRIERMCEAEGTVS 868
DB 713 CPDCCPAMVYALMIECWNEFPSPRRPRFEDHSRL-----RAMGNILS 753

RESULT 5
TRKB_MOUSE STANDARD; PRT; 821 AA.
AC P15209;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE BDNF/NT-3 growth factors receptor precursor (BC 2.7.1.112) (TrkB
DE tyrosine kinase) (GPI45-TrkB/GP95-TrkB) (TrkB-B).
GN NTRK2 OR TRKB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (GP145).
RC TISSUE=Brain;
RX MEDLINE=90059970; PubMed=2555172;
RA Klein R., Parada L.F., Coulier F., Barbacid M.;
RT "trkb, a novel tyrosine protein kinase receptor expressed during
RT mouse neural development."
RL EMBO J. 8:3701-3709(1989).
RN [2]
RP SEQUENCE FROM N.A. (GP95/Tr1).
RC TISSUE=Brain;
RX MEDLINE=90263089; PubMed=2160854;
RA Klein R., Conway D., Parada L.F., Barbacid M.;
RT "The trkb tyrosine protein kinase gene codes for a second neurogenic
RT receptor that lacks the catalytic kinase domain."
RL Cell 61:647-656(1990).
RN [3]
RP FUNCTION.
RX MEDLINE=91249395; PubMed=1645620;
RA Soppet D., Escandon E., Maragos J., Middlemas D.S., Reid S.W.,
RA Blair J., Burton L.E., Stanton B.R., Kaplan D.R., Hunter T.,
RA Nicolics K., Parada L.F.;
RT "The neurotrophic factors brain-derived neurotrophic factor and
RT neurotrophin-3 are ligands for the trkb tyrosine kinase receptor."
RL Cell 65:895-903(1991).
CC -I- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
CC NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
CC (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
CC NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
CC SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
CC GAMMA-1.
CC -I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -I- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS: AT LEAST THREE FORMS ARE PRODUCED BY
CC ALTERNATIVE SPLICING; THESE ARE: GPI45-TRKB, T1 (GP95-TRKB) AND
CC T2.
CC -I- TISSUE SPECIFICITY: THE DIFFERENT FORMS ARE DIFFERENTIALLY
CC EXPRESSED IN VARIOUS CELL TYPES. THE T2 ISOFORM IS PRIMARILY
CC EXPRESSED IN NEURONS.

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CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.  
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-  
 CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).  
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M33385; AAA0482.1; -  
 DR EMBL: X17647; CAA35636.1; -  
 DR PIR: S06943; S06943.  
 DR PIR: A35104; A35104.  
 DR HSP: P1362; 1FCX.  
 DR MGD: MGI:97384; NTRK2.  
 DR InterPro: IPR000719; Euk\_PKinase.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003598; Ig\_C2.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Cterm.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR InterPro: IPR002011; Receptor\_Tyr\_Kin\_II.  
 DR InterPro: IPR001245; Tyr\_PKinase.  
 DR Pfam: PF00047; 1g; 1.  
 DR Pfam: PF00560; LRR; 1.  
 DR Pfam: PF01462; LRRNT; 1.  
 DR Pfam: PF00069; Pkinase; 1.  
 DR PRINTS: PR00109; TYRINASE.  
 DR SMART: SM00408; IGC2; 1.  
 DR SMART: SM00082; LRCT; 1.  
 DR SMART: SM00013; LRNT; 1.  
 DR SMART: SM00219; Tyrc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transferrase: Tyrosine-protein kinase: Transmembrane; ATP-binding;  
 KW Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;  
 KW Leucine-rich repeat; Repeat; Immunoglobulin domain;  
 KW Alternative splicing.  
 FT STINAL 1 31  
 FT CHAIN 32 821  
 FT DOMAIN 32 429  
 FT TRANSMEM 430 453  
 FT DOMAIN 454 821  
 FT REPEAT 72 93  
 FT REPEAT 96 117  
 FT DOMAIN 214 270  
 FT DOMAIN 301 365  
 FT DOMAIN 537 806  
 FT NP\_BIND 543 551  
 FT BINDING 571 571  
 FT ACT\_SITE 675 675  
 FT MOD\_RES 515 515  
 FT MOD\_RES 701 701  
 FT MOD\_RES 705 705  
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FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).  
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 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPIC 466 476 PASVINDDS -> FVLEHKLPLDQ (IN  
 FT VARSPIC 477 821 MISSING (IN ISOFORM GP95-TRKB/T1).  
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 Query Match 18.9%; Score 862; DB 1; Length 821;  
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 Matches 259; Conservative 121; Mismatches 254; Indels 276; Gaps 34;  
 QY 34 LETVDALVEEATFMCVAVSYPQPEISWTNRKLIKLPDRYSIRE-----NGO 82  
 DB 96 LFTVDSGLKFEVA-YKAFKLNLSNLRHINFTNRKL-----TSLSRFRPHLDLSDLLTGN 148  
 QY 83 -----LTIISVEDSD--GIYCTANN--VGAVESGALQVKKPKITRP 126  
 DB 149 PFTSCDLMKLTLOETKSSPTQDLYCLNSESKNPLANLOIPNCGL-----PSARLA 202  
 QY 127 PIVKIIIEGLKAVLPCTTGNPKPSVMTKGD--SPLRENSIANLVESGSLRIHNVQKE 183  
 DB 203 APRLYVEEKSVTLSGSGVDGDEPLTYDVGNLVSKHMETSH--TGSLRITNISD 258  
 QY 184 DAG-QYRCVAKNSLGTAVSKV-VKLEFEVARIIRAPESHN--VYFGSFTVLHCAATGI 238  
 DB 259 DSGKQISCAENLVGDDQSVNLTGFAPRTIFLESPTSDDHMCIP-----TYRGN 310  
 QY 239 PVPITMIENGNAVSSGSIQESVKDRVIDR-----LQFTKP-----GLYTCTATNKH 288  
 DB 311 PKPALQWYNG-AALLESKYICTKHVNTHTYHGLDQ--DNPTHMNGDITLAKKNKY 367  
 QY 289 GEKSTAKAAATISIAEMSKPQDNKGYCAOYRGECNVAFLAKDALVFLNTSVADPEAQ 348  
 DB 368 G-----KDERQISAHNMG----- 380  
 QY 349 ELLVITANNELVSPVCPRAEALLCHIFQESGPGVPTPIPCREYGLAVKEFCAR 408  
 DB 381 -----RPGVD-----YETNP-----NYPEVLVE----- 398  
 QY 409 EWLVAEEKTHRLGYRSEMHLLSVPCSKLPSHMMDPTACARLPHLDYKNEKTKTPRMTS 468  
 DB 399 DWT-----PTDIGTT-----NKS----- 414  
 QY 469 SKPSVDIPNLSSSSSSFSVSPTYSMTVIISMSFAIFVLTITTLVCCRKKOMKMK 528  
 DB 415 ELPSTDVAD--QSNREHLSV--YAVVVIASVVG--FCLLMVLLKLKARHSFGMK 465  
 QY 529 RESAVALTTLTLPSELLRLRHPNMYO-----RHPLLNKL 565  
 DB 466 PASV-----ISNDDASAPLHHSNGSNTPSSSEGGDAVIIGMTKIPVENOY 515  
 QY 566 LSL-----EYPRNNIEVVRDIGEAGFGRFQARAGLLPYEPPTVAVKMKE 613  
 DB 516 FGITNSQLKPTFVOHRIKRHNIVLKRLEGEGAFGLVLAECYNLCRBDKTLVAVKTKL- 574  
 QY 614 EASADMADQFQREALMAEFDPNIVKLLGYCAVKGPKCLLFETWAYVDLNEFLRSNPH 673  
 DB 575 DASDAARDFERELLNQLQHEHIVKYGVCVEDBPLIMVEFYMKHGDLLKFLRAHPD 634  
 QY 674 TVCSLSHSDLSMRQVSSGPP--LSCABDLCIAROVAAAGAVLSEKKFVHRDLATPNC 731  
 DB 635 AV-----LMAEGNPPELTOSQMLHIAQIQAAGVYLIASQHFVRDLATPNC 681  
 QY 732 LVGENAVVYKADFGLSRNIYADYYKANENDAIPIRMWPPSIFENRYTTESDWAYGVV 791  
 DB 682 LVGENLVKLTIGDFGMSRVDYSTDYRVGGHMLPIRMWPPSIVYRKTTESDVMISLGVV 741  
 QY 792 LMEIFSGIQQYGMAMHEVIYIVRDGNIILSCPENCPVELYNLMRLCKSKLPADRPSTS 851

[illegible][illegible]

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FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 467 477 PASVISNDDS -> FVLPHKIPLDG (IN TRUNCATED
FT VARSPLIC 478 822 ISOFORM).
FT VARSPLIC 478 822 MISSING (IN TRUNCATED ISOFORM).
FT VARIANT 338 338 N -> Y (IN DBSNP:1047856).
FT SEQUENCE 822 AA, 91998 MW, 2FE915948FD013 CRC64;
SQ

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Query Match 18.8%; Score 861; DB 1; Length 822;  
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 Matches 253; Conservative 115; Mismatches 269; Indels 222; Gaps 30;

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OY 59 ISSTRKILIKLEDTRYSTRENQQL-----TILVEDSD--GIYCGT 100
DB 120 INTRNK-LTSLSRKHRLDISELTVGNPFTGCDIMWIKLOBAKSSPTODLYCLN 178
OY 101 ANNG-----VGAVESGALQVKKPKITRPINVKITIEGKAVLPCTTGPNKPSVSWIK 156
DB 179 ESKNIPLANLOIPNCGL-----PSANLAARPLTVEBCKSTLSCSVAGDPVPMYMDV 232
OY 157 GD---SPLAENSRIVLESGLRHNVQKEDAG-QYRCYAKNSLGTAYSKV-VKLEFEYF 211
DB 233 GNLVSKHNMETSH---TQSLRITNISDSDGKQISCAVENLYGHDQSVNLTVHFAPT 288
OY 212 ARILRAPESHN---VTFGSFVTLHCTATGIPVPTIWMINGNAVSGSIOESVKRVIDS 268
DB 289 IFFLESPTDHMCIF-----TVKGNPKPALOMFYNG-ALLESRYICTKIHVTNH 339
OY 269 R-----LOLEITKP-----GLYTCIATNKG--EKFSKAATISIAEMSPQ-----K 311
DB 340 TEYHCLQL--DNPTHMNGDYTLIAKNEXGKDEKQISAHFGWPGIDGANDPNPDVY 397
OY 312 DKNGCAOYRGECNAVALAKDALVFLNLSYARPEEQELVITANNEKYSPVCPRAAE 371
DB 398 EBYGTANDIDGTYNR-----SNEIPSTDVDTKTRHLSYVAVYVAVG----- 444
OY 372 ALLCNHIFOECSPPGVVPTPIPCREYCLAVELFCAKEMLVMEKTHRLYSEMHILSY 431
DB 445 -----FCL-----LVN-----LFLKL 456
OY 432 PKCSKL-----PS--MHNDPTACARPLHLDYKNEIKTTPPMSTSSKPSVDIPNLPSSSSS 485
DB 457 ARHSKFGKGPASVISNDDSDASPLHHSNGS-----NTPSSSEGG 497
OY 406 FVSPTSMTVILISNSFAIFVLLTTLTYCCRRKQKMKKRSAAVTLTLPSELL 545
DB 498 -----PDAVITGMTKP----- 509
OY 546 DRLHNPYQKMP-LLNLPKLSLEYPRNNIEYVNDIGEGAGRFQARAPGLRYEPPT 604
DB 510 --VIENPQYFITNSQLPDTFVQHIKRNHNYLKLRELGEGAKVFLAECYNLCEQOKI 567
OY 605 MVAVMYLEEASADMOQFOREAALMAEFDNPNYKLLGYCAVGRPKMLLEFYAYIGLN 664
DB 568 LVAVYTLK-DASDNARKRFHEAELITLNLQHEHNYKRYGVCESGPLLMVEYKMGDLN 626
OY 665 EPLKMSPHYVCSLSHSDLSKRAOYSPGPPP--LSCAEQLCIARQVANAAYISERKFV 722
DB 627 KFLRHGPDVAV-----LMAEGNPTELTQSOMHINOIAAGVYILASQHFV 673
OY 723 HRDLATRCVLGENNVYKIAFGLSRNIYSADYKANKANDAIPIRMPPESTFYRRTTE 782
DB 674 HRDLATRCVLGENNLVIGFGMSRDVYSTDYRVGCHTMLPIRMPPESTIMRKFTTE 733
OY 783 SDVAYGVVLEIFSYGLQPYRYGMAHEEVIYVRDGNLTSCPEKCPVLYLMLRCLWSKL 842
DB 734 SDVMSLGVVLEIFTYGQPYRYGMAHEEVIYVRDGNLTSCPEKCPVLYLMLRCLWSKL 793
OY 843 PADRPSTFSTIRLIERMCE 861

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DB 794 PHMRKNIGITHTLLOMLAK 812
RESULT 7
TRKB.CHICK
ID TRKB.CHICK STANDARD: PRT; 818 AA.
AC Q91967; Q91010;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE BDNF/NT-3 growth factors receptor precursor (EC 2.7.1.112) (TrkB
DE tyrosine kinase) (TrkB-B).
GN TRKB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=95047511; PubMed=7959025;
RA Vinh N., Erdmann K., Heumann R.;
RT "Cloning and sequence analysis of a cDNA encoding a novel truncated
RL form of the chicken TrkB receptor.";
RN Gene 149:383-384(1994).
RN (2)
RN SEQUENCE FROM N.A.
RX MEDLINE=94116452; PubMed=8287802;
RA Dechant G., Biffo S., Okazawa H., Kolbeck R., Potgiesser J.,
RA Barde Y.A.;
RT "Expression and binding characteristics of the BDNF receptor chick
RL trkB".
RL Development 119:545-558(1993).
CC -1- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),
CC NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT NERVE GROWTH FACTOR
CC (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE
CC NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN
CC SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-
CC GAMMA-1 (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: A TRUNCATED NON-CATALYTIC FORM WHICH
CC FUNCTION REMAINS STILL UNCLEAR IS PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC
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CC
DR EMBL; X77251; CAAS44468.1; -
DR EMBL; X77252; CAAS44469.1; -
DR EMBL; X74109; CAAS2210.1; -
DR HSSP; P11362; IGTI
DR InterPro; IPR000719; Euk_kinase.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR000483; LRR_Cterm.
DR InterPro; IPR000372; LRR_Nterm.

```

DR InterPro: IPR002011; Receptor\_tyr\_kin\_II.  
 DR InterPro: IPR001245; Tyr\_kinase.  
 DR Pfam: PF00047; 1g; 1.  
 DR Pfam: PF00560; LRR; 1.  
 DR Pfam: PF01463; LRRCT; 1.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PRO0109; TYRKINASE.  
 DR SMART: SM00408; IGC2; 1.  
 DR SMART: SM00082; LRRCT; 1.  
 DR SMART: SM00013; LRRNT; 1.  
 DR SMART: SM00219; TYRKC; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 DR Transferrase; Tyrosine-protein kinase; Transmembrane; ATP-binding;  
 KW Phosphorylation; Receptor; Glycoprotein; Neogenesis; Signal;  
 KW Leucine-rich repeat; Repeat; Alternative splicing;  
 KW Immunoglobulin domain;  
 FT CHAIN 1  
 FT STGNL 31  
 FT DOMAIN 32 818  
 FT TRANSMEM 32 426  
 FT DOMAIN 427 450  
 FT DOMAIN 451 818  
 FT REPEAT 71 92  
 FT REPEAT 95 116  
 FT DOMAIN 213 269  
 FT DOMAIN 300 364  
 FT DOMAIN 534 803  
 FT NP\_BIND 540 548  
 FT BINDING 568 568  
 FT ACT\_SITE 672 672  
 FT MOD\_RES 512 512  
 FT MOD\_RES 698 698  
 FT MOD\_RES 702 702  
 FT MOD\_RES 703 703  
 FT MOD\_RES 813 813  
 FT SITE 512 512  
 FT SITE 813 813  
 FT SITE 813 813  
 FT CARBOHYD 66 66  
 FT CARBOHYD 94 94  
 FT CARBOHYD 120 120  
 FT CARBOHYD 199 199  
 FT CARBOHYD 204 204  
 FT CARBOHYD 226 226  
 FT CARBOHYD 253 253  
 FT CARBOHYD 287 287  
 FT CARBOHYD 324 324  
 FT CARBOHYD 337 337  
 FT CARBOHYD 408 408  
 FT CARBOHYD 462 462  
 FT VARSPLIC 521 818  
 FT SEQUENCE 818 AA; 91736 MW; 152 CRC64;  
 Query Match 18.88; Score 858; DB 1; Length 818;  
 Best Local Similarity 29.48; Pred. No. 6.5e-50;  
 Matches 262; Conservative 118; Mismatches 281; Indels 230; Gaps 35;  
 QY 6 NIPVHI-LTIVAFSGTEKLPKAPVITPLTVDALVEVATFMCAVESYPOPEISWTRN 64  
 DB 113 NINQIYINSSKSLKSPFRHGLSLIVD-----NPKKSC-----ELMKK- 159  
 QY 65 KILKLPDTRYSIRENGOLLTILVEDSDGICTANNVGVAGVSGALQVKK----- 120  
 DB 160 -----KFOETK-----YTEAD-ICYVDNN-----KRALDMKVPNCDL 195  
 QY 121 PKTRPPINVKIIEGLKAVLCTGTMGNPKPSVSWI-----KGDSPLENSRIAVLES 174

DB 196 PSANLSNNTYVEGKSTLYCOTTCGPPPNVSWVLNLSVNSHEDTSKN-----PAS 248  
 QY 175 LRHNQKEDAGQY-RCVAKNSLGTAVSKYVLEFEVFAIRLAPSHVTCSEFYT----- 230  
 DB 249 LITKIVSSMDSGMLSCVAVENIVEYQVSA---ELTVF-----AP---NITFEESTPPH 298  
 QY 231 ---LHCATGIPVPTITWENGNAVSGSIOESVCKRVIDSR-----LOLETKP----- 277  
 DB 299 HMCIPFTVKGKPKPTQWTFEG-AIINSEYICOTKHIVINOSYHGCLOD---DNPTHNN 355  
 QY 278 GLYTCTATNKGKFEFTAKAATISIAENSKPOKDNKGYCAQY---GEVCNAVLAOKDL 334  
 DB 356 GAVTLAKNEYGE-----DEKRDAPHMSVPGDSGPIVDPDY 394  
 QY 335 VFLNTSGADEEAOELLVHTANMLKVSP-VCPAAEALCHNIFQESPGVPTPIPI 393  
 DB 395 EYETT-----PND-----LGDITNNSNOTSPVSNKEHEDSITYV-----VGTALV 439  
 QY 394 CREYCLAVKELFCAKEWLVMEKTHRGLYRSEHMLLVPCSKLPS--MHMDPTACARLP 451  
 DB 440 CTGLVIML-----ILKFGH-----SKFGM-----KGPSVISDSDSAPLH 478  
 QY 452 HLDYKNENLKPPTMTSSKPSVDIPNLPSSSSSFSVPTYSMTVIISMSFAIVLT 511  
 DB 479 HISNGS-----NTPSSSEG----- 493  
 QY 512 ITTLCCRRKKKMKKRESAAVLTLPSELDDLRLHPNMYORMP-LILNPKLLSLEY 570  
 DB 494 -----PDVITGMTKIP-----VIENPOFGITNSQDKPDTPFOHI 529  
 QY 571 PRNIEYRDIGEGAFGRVFOARAPGLPYEPPTMAVAKMLKEPASADQADQREALM 630  
 DB 530 KRHNIVLRELHGEAFGLVLAECYNLCPEODKLIVAVKTLK-DASNARKDHREKELL 588  
 QY 631 AEPNPVIVLLGCAVCAKGMCLFEYMAVGDNEFLRSMSPHYTCLSHSDLSMARQVS 690  
 DB 589 TNLQHEHIVKRYGVCEVDPLIMVEYMKHDLKFLRAIGPDV-----LMAE 637  
 QY 691 SPGPPLSCAEOLCIAQVAVAGNAVYLSERRFHRDLATRCNLGVENNVAIADGSLRN 750  
 DB 638 GNRPAELTQSGMLHIAQVIAAGVYLASQHFVHDLATRCNLGVENLVIGFGMSRDV 697  
 QY 751 YSADYYANENDAIPIKMPPEISFYKRYTTESVYAVGVLLMEISFYGLOPYGAAHEE 810  
 DB 698 YSTDYVIRGGTJMPKIMMPESIMYKRTTESVMSLVGLVMEIFYGKOPWIOISNE 757  
 QY 811 VTYVVRGNIISCPCNPVELYNLMRLCWSKLPADREPSYSIRLRBMCE 861  
 DB 758 VIECITQGRVLRRTCPKEVYDLMGQWQREPHMLRIKTHSLONLAK 808  
 RESULT 8  
 TRKB\_RAT STANDARD; PRT; 821 AA.  
 ID TRKB\_RAT  
 AC 063604: 063605: 063606:  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE BDNF/NT-3 growth factors receptor precursor (BC 2.7.1.112) (TrkB  
 DE tyrosine kinase) (GPI45-TrkB/GP95-TrkB) (TrkB-B).  
 GN NTRK2 OR TRKB.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN (1)  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC TISSUE=Cerebellum;  
 RX MEDLINE=91094826; PubMed=1846020;  
 RA Middlemas D.S., Lindberg R.A., Hunter T.;  
 RT "trkb, a neural receptor protein-tyrosine kinase: evidence for a  
 full-length and two truncated receptors.";



RL Mol. Cell. Biol. 11:143-153(1991).  
 RN [2]  
 RP PHOSPHORYLATION SITES.  
 RX MEDLINE-94149017; PubMed-8106527;  
 RA Middelmas D.S., Meisenhelder J., Hunter T.:  
 RT "Identification of TrkB autophosphorylation sites and evidence that  
 RT phosphotyrosine C gamma 1 is a substrate of the TrkB receptor.";  
 RT J. Biol. Chem. 269:5458-5466(1994).  
 CC -1- FUNCTION: RECEPTOR FOR BRAIN-DERIVED NEUROTROPHIC FACTOR (BDNF),  
 CC NEUROTROPIN-3 AND NEUROTROPIN-4/5 BUT NOT NERVE GROWTH FACTOR  
 CC (NGF). INVOLVED IN THE DEVELOPMENT AND/OR MAINTENANCE OF THE  
 CC NERVOUS SYSTEM. THIS IS A TYROSINE-PROTEIN KINASE RECEPTOR. KNOWN  
 CC SUBSTRATES FOR THE TRK RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-  
 CC GAMMA-1.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW  
 CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; GP145-TRKB (SHOWN  
 CC HERE), T1/GP95-TRKB AND T2; ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: THE DIFFERENT FORMS ARE DIFFERENTIALLY  
 CC EXPRESSED IN VARIOUS CELL TYPES. THE T2 ISOFORM IS PRIMARILY  
 CC EXPRESSED IN NEURONS.  
 CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.  
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-  
 CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).  
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC  
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 CC  
 CC EMBL: M55291; AAA42279.1; -;  
 CC EMBL: M55292; AAA42280.1; -;  
 CC EMBL: M55293; AAA42281.1; -;  
 CC HSSP: P1362; IAGM.  
 CC InterPro: IPR000719; Euk\_Pkinase.  
 CC InterPro: IPR003006; I9\_MHC.  
 CC InterPro: IPR003598; I9\_C2.  
 CC InterPro: IPR001611; LRR.  
 CC InterPro: IPR000483; LRR\_Cterm.  
 CC InterPro: IPR000372; LRR\_Nterm.  
 CC InterPro: IPR002011; Receptor\_tyr\_kin\_II.  
 CC InterPro: IPR001245; Tyr\_Pkinase.  
 CC Pfam: PF00047; 1g; 1.  
 CC Pfam: PF00560; LRR; 1.  
 CC Pfam: PF01463; LRRCT; 1.  
 CC Pfam: PF01462; LRRNT; 1.  
 CC Pfam: PF00069; Pkinase; 1.  
 CC PRINTS: PR00109; TYRKINASE.  
 CC SMART: SM00408; IGC2; 1.  
 CC SMART: SM00082; LRRCT; 1.  
 CC SMART: SM00013; LRRNT; 1.  
 CC SMART: SM00219; TYRKT; 1.  
 CC PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 CC PROSITE: PS00109; RECEPTOR\_TYR\_KIN\_II; 1.  
 CC PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 CC PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 CC Transferrase: Tyrosine-protein kinase; Transmembrane; ATP-binding;  
 CC Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;  
 CC Leucine-rich repeat; Repeat; Immunoglobulin domain;  
 CC Alternative splicing;  
 CC SIGNAL 1 31 BY SIMILARITY.  
 CC CHAIN 32 821 BDNF/NT-3 GROWTH FACTORS RECEPTOR.  
 CC DOMAIN 32 429 EXTRACELLULAR (POTENTIAL).  
 CC TRANSMEM 430 453 POTENTIAL.  
 CC DOMAIN 454 821 CYTOPLASMIC (POTENTIAL).

FT REPEAT 72 93 LRR 1.  
 FT REPEAT 96 117 LRR 2.  
 FT DOMAIN 214 270 IG-LIKE C2-TYPE DOMAIN 1.  
 FT DOMAIN 301 365 IG-LIKE C2-TYPE DOMAIN 2.  
 FT DOMAIN 537 606 PROTEIN KINASE.  
 FT NP\_BIND 543 551 ATP (BY SIMILARITY).  
 FT BINDING 571 571 ATP (BY SIMILARITY).  
 FT ACT\_SITE 675 675 BY SIMILARITY.  
 FT MOD\_RES 515 515 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 701 701 PHOSPHORYLATION (AUTO-).  
 FT MOD\_RES 705 705 PHOSPHORYLATION (AUTO-).  
 FT MOD\_RES 706 706 PHOSPHORYLATION (AUTO-).  
 FT MOD\_RES 816 816 PHOSPHORYLATION (AUTO-).  
 FT SITE 515 515 INTERACTION WITH SHC PROTEIN (BY SIMILARITY).  
 FT SITE 816 816 INTERACTION WITH PLC-GAMMA-1 (BY SIMILARITY).  
 FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPPLIC 466 476 PASVSNDDDS -> FVLFHKKPLDGG (IN ISOFORM T1).  
 FT VARSPPLIC 477 821 MISSING (IN ISOFORM T1).  
 FT VARSPPLIC 466 474 PASVSNDD -> KGCACAFAS (IN ISOFORM T2).  
 FT VARSPPLIC 475 821 MISSING (IN ISOFORM T2).  
 SQ SEQUENCE 821 AA; 92186 MW; 0DDACDA212CDA0E CRC64;  
  
 Query Match 18.7%; Score 854.5; DB 1; Length 821;  
 Best Local Similarity 28.3%; Pred. No. 1;le-49;  
 Matches 249; Conservative 113; Mismatches 254; Indels 263; Gaps 30;  
  
 QY 59 ISWTRNKILIKLFDTRYISIRE-----NGQ-----LLTILSVSDSD--G 95  
 DB 120 INFTRNKL-----TSLSRHRRHLDLSLILTGNPFTSCDLMWTKTLQETKSSPDTD 173  
 QY 96 IYVCTANN-----VGAVESCGALQYMKPKITRPINVKIIEGLAVLPCTMGNPKPS 151  
 DB 174 LYCLNNSKNTPLANLIQINCGI-----PSARLAPNLFVEBGSVITISCSVGDPLPT 227  
 QY 152 VSMIKGD-----SPRENSKRLAVLESGLRIHNOKEAG-QYRVANNSGTATASV-VKL 206  
 DB 228 LYWDVGNILVSKHNETSH-----TQGLRRTINISSDSGKQISCAVNLVGEODDSVNLTV 283  
 QY 207 EEFVFAIRLAPESHN---VTFGSFVTLHCTATGIVPTTIWENNAVSSGSIQSVSD 263  
 DB 284 HRAPTTFLESPISDHMKIIP-----YRGNKPRLQWYNG-ALINSEKYICTKI 334  
 QY 264 RVIDSR-----IQLTFRK-----GLYCIATNKGK-----KFSYAKAA 298  
 DB 335 HTYNNHTEYHGLIOL--DNPTTHMNNGDYTLMAKREYKDEKROISAHNMGKRGVDETNPV 392  
 QY 299 ATISTAEKSKP-----QDKNGYCAQYRGECVNAVLAKDALVPLNTSYADEEEOQL 351  
 DB 393 PEVLVEDWTPPDIDGTIKSNSE-----IPSTVDADOTNREHNS 431  
 QY 352 VHTANMELVSPVPCRAEALLCNHIFQECSPGVVPTPIPCREYCSLAVKELFCAKEM 411  
 DB 432 VYAVVVIASVVG-----FCLLYML----- 451  
 QY 412 VMEKTRHRLYSEHMLLVPRCKSL---PS--MHMDPTACARLPHLDYKNENLKTFRP 465  
 DB 452 -----LKLARHSKFGMKGRASVINDSDASPLRHISNGS----- 487  
 QY 466 MTSKSKSVIPNIPSSSSSSFSVSPYISMTVIISMSFAIFVLLITTLTYCCRRKKOMK 525





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FT CHAIN 32 827 NT-3 GROWTH FACTOR RECEPTOR.
FT DOMAIN 32 430 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 431 455 POTENTIAL.
FT DOMAIN 456 827 CYTOPLASMIC (POTENTIAL).
FT REPEAT 102 125 LRR 1.
FT REPEAT 126 149 LRR 2.
FT DOMAIN 227 288 IG-LIKE C2-TYPE DOMAIN 1.
FT DOMAIN 319 382 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 340 382 PROTEIN KINASE.
FT NP_BIND 546 554 ATP (BY SIMILARITY).
FT BINDING 574 574 BY SIMILARITY.
FT ACT_SITE 681 681 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 518 518 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 707 707 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 711 711 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 712 712 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 822 822 INTERACTION WITH SHC PROTEIN (BY SIMILARITY).
FT SITE 518 518 INTERACTION WITH PLC-GAMMA-1 (BY SIMILARITY).
FT SITE 822 822 INTERACTION WITH PLC-GAMMA-1 (BY SIMILARITY).
FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 375 375 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 98 MISSING (IN BETA EXTRACELLULAR MOTIF).
FT VARSPLIC 581 619 LAAKRDQRAEELITNIQHEHYKFGVCGDPLNIFV
-> CFEIMLNPISTLPGHSGPLNGLIVEDEVYSKGRHG
F (IN ISOFORM KD).
FT VARSPLIC 620 827 MISSING (IN ISOFORM KD).
FT VARSPLIC 633 664 AHGPDAMILVDGPRKAGELGSLQMLHIASQ -> LEDTP
CCLSGAGLRASCTGSSGRVTSAGS (IN ISOFORM
KT).
FT VARSPLIC 665 827 MISSING (IN ISOFORM KT).
FT VARSPLIC 713 713 R -> REGPRKQSLSTAWQRHRLAPPAAT (IN
ISOFORM K125).
FT CONFLICT 1 39 MDVSLPTCKCTFWRFVLLMSIMGDIYLSVACPAACLS
-> MHWCRIFASDRKLVF (IN REF. 2).
FT CONFLICT 124 124 A -> G (IN REF. 2).
FT CONFLICT 378 378 I -> P (IN REF. 3).
FT CONFLICT 481 496 SPLHHNHGITTSSL -> AHTSTTDTTRFVT (IN
REF. 2).
FT CONFLICT 795 795 W -> C (IN REF. 2).
FT SEQUENCE 827 AA; 93180 MW; AB97373113DCB28A CRC64;
SQ

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Db 245 VADLHSINTHQNLNMTNVAHNLITLVNVTSEDNGLFLLCIAENVGMSNASVL-LTVVY 303
Qy 211 FARLRAPD-----SHWVTGSEVTLTCTATGILPVITITENGNAV-----SS 254
Db 304 PPRLLTLEEVLEHLEHIAF-----AVH-----GNAPLTHLHNGOVLREPIITHEFTYQ 355
Qy 255 GSTIOESKDVIDSRLQFLTTP-----GLYCIATPKHGEKSTAKAATISIAESKP 309
Db 356 GEVSEGC-----LNNKPTHHNNGVITIVATNQGLSANTQITIG----- 393
Qy 310 QKDNKGYCAQYRGCEVCNAVLAKDALVPLNTSYADPEAQELVHTAMNELKVSPVCRPA 369
Db 394 ----- 393
Qy 370 AEALCNHINQDESPGVPPPIPIREYCLAVKELFCAKEMLVMEKTHRGVREMHLL 429
Db 394 -----HFL 396
Qy 430 SVPKCSKLPSMHMDPTACARLPHLDYKNELKTPPMTSKSPSYDIPNLPSSSSSPSVS 489
Db 397 EKP-----FPESTDNFVSI-----GDYEVS 416
Qy 490 PTSMATYI-----ISTMSFAIFVLLITITLYCC-----RRRKQMKK-----KR 529
Db 417 PTPPTITHKPEEDDFGVSIAVGLAFAVLLVFLTMINKYGRKSGFMKGPAVATSGE 476
Qy 530 ESAAVTL-----TTLSELLDLRLHNPMP-----YQRPDLNPLKLSLEY----- 570
Db 477 EDSASPLHHNHGITTSSL-----DAGPDIVYIGTRPIVENPQYFGHNCCHKPDYVQ 533
Qy 571 --PNNIETVYRDIGEGAFGRVQARAGLLPYEFTVAVAKMLKEASADMDQFOEEA 628
Db 534 HIKRRDYLVRKELEGAFGRVFAECYNLSPTNDKMLVAVAKALDPLA-ARKDFOEAE 592
Qy 629 LMAEFDNPNIYKILGYCAVGRKMCLLFEYVAGDLEFLMSPEHTVCSLSHSDLSMRAQ 688
Db 593 LITLQHEHYIKFYGVCGDDPLINVEYMKHGNLFLAHGPD-----AM 639
Qy 689 VSSGPP-----PLSCAEQICIAQVANAAYLSERKFVHRDLATRCNLGVENNVYIAD 743
Db 640 ILVVGPRQAKAGELGLSOMLIASQIASGMVYLLASHQFVHDLATRCNLGVANLIVIGD 699
Qy 744 FGLSRNITSADYKXANNDAPIRWMPSESTFYRYTSTESVMAVGVVMEIFSYGLQPY 803
Db 700 FGMSRDVYSTDYVVGVTMLPIRMWPESTIMTKFTTESDVSFGYILMIFITYGQWP 759
Qy 804 YGMAHEEYIVYVRGNILISCPENVLYLMLRLCKSLPADRPSFTSHIRILERM 859
Db 760 FQLSNTEVIEICITGGRVLERPRVCPKEVYDMLGCMQREPOQRINIKIYKILHAL 815

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RESULT 11
TRKA_HUMAN
ID TRKA_HUMAN STANDARD; PRT; 796 AA.
AC P04629; P08119; Q9U107;
DT 13-AUG-1987 (Rel. 05, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE High affinity nerve growth factor receptor precursor (EC 2.7.1.112)
DE (TRK1 transformatory tyrosine kinase protein) (p140-TRK) (Trk-A).
GN NTRK1 OR TRK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (TRKA-I ISOFORM).
RC TISSUE=Colon.
RX MEDLINE=89181575; PubMed=2927393.
RA Martin-Zanca D., Oskam R., Mitra G., Copeland T.D., Barbacid M.;
RT "Molecular and biochemical characterization of the human trk proto-
oncogene.";
RL Mol. Cell. Biol. 9:24-33(1989).

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RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Brain;  
 RA MEDLINE-95123473; PubMed-7823156;  
 RA Shelton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P.,  
 RA Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;  
 RT "Human trks: molecular cloning, tissue distribution, and expression  
 RL of extracellular domain immunoadhesins.";  
 RL J. Neurosci. 15:477-491(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97435581; PubMed-9290260;  
 RA Indo Y., Mardy S., Tsuruta M., Karim M.A., Matsuda I.;  
 RT "Structure and organization of the human TRKA gene encoding a high  
 RL affinity receptor for nerve growth factor.";  
 RL Jpn. J. Hum. Genet. 42:343-351(1997).  
 RN [4]  
 RP SEQUENCE OF 399-796 FROM N.A.  
 RX MEDLINE-86146854; PubMed-2869410;  
 RA Martin-Zanca D., Hughes S.H., Barbacid M.;  
 RT "A human oncogene formed by the fusion of truncated tropomyosin and  
 RL protein tyrosine kinase sequences.";  
 RL Nature 319:743-748(1986).  
 RN [5]  
 RP SEQUENCE OF 399-796 FROM N.A.  
 RX MEDLINE-88196074; PubMed-2966065;  
 RA Kozma S.C., Redmond S.M.S., Saurer S.M., Groner B., Hynes N.E.;  
 RT "Activation of the receptor kinase domain of the trk oncogene by  
 RL recombination with two different cellular sequences.";  
 RL EMBO J. 7:147-154(1988).  
 RN [6]  
 RP FUNCTION.  
 RX MEDLINE-91218846; PubMed-1850821;  
 RA Hemstead B.L., Martin-Zanca D., Kaplan D.R., Parada L.F., Chao M.V.;  
 RT "High-affinity NGF binding requires coexpression of the trk proto-  
 RL oncogene and the low-affinity NGF receptor.";  
 RL Nature 350:678-683(1991).  
 RN [7]  
 RP FUNCTION.  
 RX MEDLINE-91191557; PubMed-1849459;  
 RA Klein R., Jing S., Nanduri V., O'Rourke E., Barbacid M.;  
 RT "The trk proto-oncogene encodes a receptor for nerve growth factor.";  
 RL Cell 65:185-197(1991).  
 RN [8]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE-93315496; PubMed-8325889;  
 RA Barker P.A., Lomen-Hoerch C., Genesch E.M., Meakin S.O., Glass D.J.,  
 RA Shooter E.M.;  
 RT "Tissue-specific alternative splicing generates two isoforms of the  
 RL trkA receptor.";  
 RL J. Biol. Chem. 268:15150-15157(1993).  
 RN [9]  
 RP MUTAGENESIS OF TYR-791.  
 RX MEDLINE-94179299; PubMed-7510697;  
 RA Loeb D.M., Stephens R.M., Copeland T.D., Kaplan D.R., Greene L.A.;  
 RT "A trk nerve growth factor (NGF) receptor point mutation affecting  
 RL interaction with phospholipase C-gamma 1 abolishes NGF-promoted  
 RL peripheral induction but not neurite outgrowth.";  
 RL J. Biol. Chem. 269:8901-8910(1994).  
 RN [10]  
 RP MUTAGENESIS AND PHOSPHORYLATION SITES.  
 RX MEDLINE-94206546; PubMed-8155326;  
 RA Stephens R.M., Loeb D.M., Copeland T.D., Pawson T., Greene L.A.,  
 RA Kaplan D.R.;  
 RT "Trk receptors use redundant signal transduction pathways involving  
 RL SHC and PLC-gamma 1 to mediate NGF responses.";  
 RL Neuron 12:691-705(1994).  
 RN [11]  
 RP STRUCTURE BY NMR OF 489-500.  
 RX MEDLINE-96097066; PubMed-8524391;  
 RA Zhou M.M., Ravichandran K.S., Olejniczak E.F., Petros A.M.,  
 RA Meadows R.P., Sattler M., Harlan J.E., Wade W.S., Burakoff S.J.,  
 RA Fesik S.W.;

RT "Structure and ligand recognition of the phosphotyrosine binding  
 RL domain of Shc.";  
 RL Nature 378:584-592(1995).  
 RN [12]  
 RP VARIANT CIPA ARG-577.  
 RX MEDLINE-96311294; PubMed-8696348;  
 RA Indo Y., Tsuruta M., Hayashida Y., Karim M.A., Ohta K., Kawano T.,  
 RA Mitsubuchi H., Tonoki H., Awaya Y., Matsuda I.;  
 RT "Mutations in the TRKA/NGF receptor gene in patients with congenital  
 RL insensitivity to pain with anhidrosis.";  
 RL Nat. Genet. 13:485-488(1996).  
 RN [13]  
 RP VARIANT CIPA PRO-780.  
 RX MEDLINE-99192367; PubMed-10090906;  
 RA Greco A., Villa R., Tubino B., Romano L., Penso D., Pierotti M.A.;  
 RT "A novel NTRK1 mutation associated with Congenital Insensitivity to  
 RL Pain with Anhidrosis.";  
 RL Am. J. Hum. Genet. 64:1207-1210(1999).  
 RN [14]  
 RP VARIANTS CIPA P-213; W-649 AND S-714, AND VARIANTS S-85; Y-604 AND  
 RP V-613.  
 RX MEDLINE-99264238; PubMed-10330344;  
 RA Mardy S., Miura Y., Endo F., Matsuda I., Sztricha L., Frossard P.,  
 RA Moosa A.G., Ismail E.A.R., Macaya A., Andria G., Toscano E., Gibson W.,  
 RA Graham G.E., Indo Y.;  
 RT "Congenital insensitivity to pain with anhidrosis: novel mutations in  
 RL the TRKA (NTRK1) gene encoding a high-affinity receptor for nerve  
 RL growth factor.";  
 RL Am. J. Hum. Genet. 64:1570-1579(1999).  
 RN [15]  
 RP VARIANTS TYR-604; VAL-613 AND GLN-780.  
 RX MEDLINE-99371280; PubMed-10443680;  
 RA Gimm O., Greco A., Hoang-Vu C., Dralle H., Pierotti M.A., Eng C.;  
 RT "Mutation analysis reveals novel sequence variants in NTRK1 in  
 RL sporadic human medullary thyroid carcinoma.";  
 RL J. Clin. Endocrinol. Metab. 84:2784-2787(1999).  
 RN [16]  
 RP VARIANT CIPA VAL-587.  
 RX MEDLINE-99250414; PubMed-10233776;  
 RA Kotsumoto S., Setoyama M., Hozumi H., Mizoguchi S., Fukumaru S.,  
 RA Kobayashi K., Sasaki T., Kanzaki T.;  
 RT "A novel point mutation affecting the tyrosine kinase domain of the  
 RL trkA gene in a family with congenital insensitivity to pain with  
 RL anhidrosis.";  
 RL J. Invest. Dermatol. 112:810-814(1999).  
 RN [17]  
 RP VARIANT CIPA LEU-695, AND VARIANT VAL-613.  
 RP TISSUE-Peripheral blood;  
 RX MEDLINE-20321341; PubMed-10861667;  
 RA Shatzky S., Moses S., Levy J., Plinsk V., Hershkovitz E., Herzog L.,  
 RA Shorer Z., Luder A., Parvari R.;  
 RT "Congenital insensitivity to pain with anhidrosis (CIPA) in  
 RL Israeli-Bedouins: genetic heterogeneity, novel mutations in the  
 RL TRKA/NGF receptor gene, clinical findings, and results of nerve  
 RL conduction studies.";  
 RL Am. J. Med. Genet. 92:353-360(2000).  
 RN [18]  
 RP VARIANTS CIPA PRO-93; ARG-522; ARG-577; CYS-654 AND TYR-674.  
 RX MEDLINE-20435070; PubMed-10982191;  
 RA Miura Y., Mardy S., Awaya Y., Nihel K., Endo F., Matsuda I., Indo Y.;  
 RT "Mutation and polymorphism analysis of the TRKA (NTRK1) gene encoding  
 RL a high-affinity receptor for nerve growth factor in congenital  
 RL insensitivity to pain with anhidrosis (CIPA) families.";  
 RL Hum. Genet. 106:116-124(2000).  
 RN [19]  
 RP VARIANT CIPA ARG-577.  
 RX MEDLINE-20036616; PubMed-10567924;  
 RA Greco A., Villa R., Fusetti L., Orlandi R., Pierotti M.A.;  
 RT "The gly571arg mutation, associated with the autonomic and sensory  
 RL inactivation of the NTRK1/nerve growth factor receptor.";  
 RL J. Cell. Physiol. 182:127-133(2000).  
 CC -I- FUNCTION: REQUIRED FOR HIGH-AFFINITY BINDING TO NERVE GROWTH

CC FACTOR (NGF), NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT BRAIN-  
 CC RECEIVED NEUROTROPHIC FACTOR (BDNF). KNOWN SUBSTRATES FOR THE TRK  
 CC RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1. HAS A CRITICAL  
 CC ROLE IN THE DEVELOPMENT AND FUNCTION OF THE NOCICEPTIVE RECEPTION  
 CC SYSTEM AS WELL AS ESTABLISHMENT OF THERMAL REGULATION VIA  
 CC SWEATING. ACTIVATES ERK1 BY EITHER SHC- OR PLC-GAMMA-1-DEPENDENT  
 CC SIGNALING PATHWAY.  
 CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC - SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW  
 CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.  
 CC - SUBCELLULAR LOCATION: TYPE I membrane protein.  
 CC - ALTERNATIVE PRODUCTS: 2 ISOFORMS; TRKA-I AND TRKA-II (SHOWN  
 CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. BOTH ISOFORMS HAVE  
 CC SIMILAR BIOLOGICAL PROPERTIES.  
 CC - TISSUE SPECIFICITY: TRKA-II IS PRIMARILY EXPRESSED IN NEURONAL  
 CC CELLS; TRKA-I IS FOUND IN NON-NEURONAL TISSUES.  
 CC - PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.  
 CC - DISEASE: THE AMINO END OF SEVERAL DIFFERENT CELLULAR PROTEINS  
 CC (SUCH AS NON-MUSCLE TROPOMYOSIN TM30NM) HAS BEEN FOUND FUSED WITH  
 CC THE PROTEIN TYROSINE KINASE DOMAIN ENCODED BY NTRK1. THESE SOMATIC  
 CC REARRANGEMENT CREATES AN ONCOGENIC PROTEIN.  
 CC - DISEASE: DEFECTS IN NTRK1 ARE A CAUSE OF A DISEASE CALLED CIPA;  
 CC WHICH IS CHARACTERIZED BY A CONGENITAL INSENSITIVITY TO PAIN,  
 CC ANHIDROSIS (ABSENCE OF SWEATING), ABSENCE OF REACTION TO NOXIOUS  
 CC STIMULI, SELF-MUTILATING BEHAVIOR, AND MENTAL RETARDATION. THIS  
 CC RARE AUTOSOMAL RECESSIVE DISORDER IS ALSO KNOWN AS CONGENITAL  
 CC SENSORY NEUROPATHY WITH ANHIDROSIS OR HEREDITARY SENSORY AND  
 CC AUTONOMIC NEUROPATHY TYPE IV OR FAMILIAL DYSAUTONOMIA TYPE II.  
 CC - SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-  
 CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.  
 CC - SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).  
 CC - SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC

Query Match 17.8%; Score 812; DB 1; Length 796;  
 Best Local Similarity 26.7%; Pred. No. 7.5e-47;  
 Matches 233; Conservative 117; Mismatches 247; Indels 330; Gaps 30;

QY 1 MRELVNIPILHILTY-----AFSGTEKLPRKAVITTPLEVDALVEEVATEMCA 50  
 DB 84 LRLRLGELRLNLTIVSGRFAVDPAHFHTPRLSRLNLFPMLES----- 129  
 QY 51 VESYPOEISWTRNKILIKLFTTRYSTRENGQLTITISVEDSDGICYCTA-----N 102  
 DB 130 -----LSW-----KTVQGLSLQELVLSGNDPLSCALRWLQWEE 164  
 QY 103 NGYGAWE-----SCGALQVKKPKITPRIVKTIIEGKAVLRPCTM 145  
 DB 165 EELGAVPEOKLQCHGGPLAHMPNASCQVPTLKVOP-----NASVDVGDVLLRCQVE 218  
 QY 146 GNEKPSVSWIKGDSPLRENSRIA-VLESQ-----SLRIHNVQKE-DAGQYRCVAKNSLGT 198  
 DB 219 GRLEQAGWI-----LTELQSATVMSKSGPLSLGLTLAVTSDLNKRLNLTQAMENDVGR 273  
 QY 199 AYKVVVKLEFEVARIIRAPESHNVTFGSVTLH-----C---TATGIPVETTWIE 247  
 DB 274 A-----EVSVOV-----NVSPFASVOLHTAVEMHMCIPFSVDGQAPASRLMLF 317  
 QY 248 NGNAVSSGS-----IOESVKRYIDSRQLDLFTKP-----GLYTCIATNKHGKGFSTAK 296  
 DB 318 NGSVLNTSTFTTEFEPRANETVRHGCRLR--NQRPHVNGNTLLAANFEGQ----- 369  
 QY 297 AATITIAIEMSKPODKNGKGYCAQYRGVCNAVLAKDALVELNTSYADPEEAQDELVHTAW 356  
 DB 370 ASASIMAAEFNDNPFEN-----PED----- 389  
 QY 357 NELKVVSPVCRPAEALLCNHIFQESPGVVPPIPICREYCAVLKELFCAKEWLVMEK 416  
 DB 390 -----PIV----- 393  
 QY 417 THRGLYRSEMHLLSVPRCKSLPSMMDPTGACARLPHLDYKKNLKTFRPMTSSKPSVDIP 476

DB 394 -----SFSPVDNTJSGD-- 406  
 QY 477 NLPESSSSFSVSPYSMTVITISMSFAIFVLTITLY-----CCRRKQWKNK----- 527  
 DB 407 PVKKEDTPEGV-----SVAVGLAVFACFLSTLLVLYNKKGRNNKFGINRAVL 456  
 QY 528 -KRESAAVTL-----TLPSE-----LLIDRLHPNPTORMPLLPKLLSLTEPRNN 574  
 DB 457 APEGLAMLSHFMFLGGSSSPTEGKSGGLGHIENEDQYFSDACVHHIK-----RSD 509  
 QY 575 IEVYRDGEAGFAGVFPARAPGLPYEPFTVAVAKMKKEESADMOADFOREALMAEFD 634  
 DB 510 IYLVKWEIGEGAFGVFLAECHNLPLPEDOKMLVAYAKLK-EASEARQDFOREALLMLQ 568  
 QY 635 NPNIYKLLGYCAVAKPKMLLFYMAAYGDLNLFKMSRPHTVCSLSHSDLSRAQVSSPGP 694  
 DB 569 HQHIVREFGYCTEGRPLLMVEYVRHGDNLFLSHGP-----DAKLLAGEDVAP 619  
 QY 695 PPLSCAQDLTIARQVAAAGMAYLSERKVEYHDLATRNCLVGENMYKTDGSLRNITYSAD 754  
 DB 620 GPLGLGLLAVASQVAAQMYLADLHFVHDLATRNCLVGGGLVVKIGDFGMSHDYSTD 679  
 QY 755 YRKANDDAIPRMPPEISIFNRYTTESDVWAGVYLMFEISYGLQPYGMAHEVYIY 814  
 DB 680 YIRGAGRTMLPIRMPPEISILYKFTTESDVWISGVYLMFEITGKQPYWOLSTMAIDC 739  
 QY 815 VRDGNLSCPEPCVELYINRLCWSKLPADRPSTSIHRIEMCE 861  
 DB 740 ITQRELEPRPRCPPEYVALIMRCQWOREPOQRHSIKIVHARLQALQ 786

RESULT 12  
 ID TRKC\_HUMAN STANDARD; PRT; 839 AA.  
 AC Q16288; Q16289; Q12827;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ntr-3 growth factor receptor precursor (EC 2.7.1.112) (TrkC tyrosine  
 DE kinase) (GPI45-TrkC) (Trk-C).  
 GN NTRK3 OR TRKC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=95123473; Pubmed=7823156;  
 RA Shelton D.L., Sutherland J., Gripp J., Camerato T., Armanini M.P.,  
 RA Phillips H.S., Carroll K., Spencer S.D., Levinson A.D.;  
 RT "Human trks: molecular cloning, tissue distribution, and expression  
 RT of extracellular domain immunoadhesins.";  
 RL J. Neurosci. 15:477-491(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=fetal brain;  
 RX MEDLINE=95104834; Pubmed=7806211;  
 RA McGregor L.M., Baylin S.B., Griffin C.A., Hawkins A.L., Nelkin B.D.;  
 RT "Molecular cloning of the cDNA for human TrkC (NTRK3), chromosomal  
 RT assignment, and evidence for a splice variant.";  
 RL Genomics 22:267-272(1994).  
 CC - FUNCTION: RECEPTOR FOR NEUROTROPHIN-3 (NT-3). THIS IS A TYROSINE-  
 CC PROTEIN KINASE RECEPTOR. KNOWN SUBSTRATES FOR THE TRK RECEPTORS  
 CC ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1.  
 CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC - SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW  
 CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES (BY SIMILARITY).  
 CC - SUBCELLULAR LOCATION: TYPE I membrane protein.  
 CC - ALTERNATIVE PRODUCTS: AT LEAST FOUR FORMS OF TRKC ARE PRODUCED BY  
 CC ALTERNATIVE SPLICING. THE DIFFERENT ISOFORMS DO NOT HAVE IDENTICAL  
 CC SIGNALING PROPERTIES. THE ISOFORM B IS EXPRESSED IN A RELATIVELY

CC LARGE AMOUNT IN THE ADULT BRAIN COMPARATIVELY TO FETAL BRAIN.  
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED, MAINLY IN THE NERVOUS  
 CC TISSUE.  
 CC -1- PFM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.  
 CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-  
 CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).  
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
 CC -----  
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 CC -----  
 DR EMBL: S76475; AAB3311.1; -  
 DR EMBL: S76476; AAB3312.1; -  
 DR EMBL: U05012; AAB75374.1; -  
 DR HSSP: P11362; IAGW.  
 DR MIM: 191316; -  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR003589; Ig.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR001611; LRR.  
 DR InterPro: IPR000483; LRR\_Cterm.  
 DR InterPro: IPR000372; LRR\_Nterm.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00047; Ig\_1.  
 DR Pfam: PF00560; LRR; 2.  
 DR Pfam: PF01463; LRRT; 1.  
 DR Pfam: PF01462; LRRT; 1.  
 DR Pfam: PF00069; pkinase; 1.  
 DR SMART: SM00409; IG; 1.  
 DR SMART: SM00082; LRRT; 1.  
 DR SMART: SM00013; LRRT; 1.  
 DR SMART: SM00219; TYRK; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS00239; RECEPTOR\_TYR\_KIN\_II; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transferrase: Tyrosine-protein kinase: Transmembrane; ATP-binding;  
 DR Phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;  
 DR Leucine-rich repeat; Repeat; Alternative splicing;  
 DR Immunoglobulin domain.  
 DR SIGNAL 1 31  
 DR CHAIN 32 839  
 DR DOMAIN 32 429  
 DR TRANSMEM 430 453  
 DR DOMAIN 454 839  
 DR REPEAT 102 125  
 DR REPEAT 126 149  
 DR DOMAIN 227 288  
 DR DOMAIN 319 382  
 DR DOMAIN 538 839  
 DR NP\_BIND 544 552  
 DR BINDING 572 572  
 DR ACT\_SITE 679 679  
 DR MOD\_RES 516 516  
 DR MOD\_RES 705 705  
 DR MOD\_RES 709 709  
 DR MOD\_RES 710 710  
 DR MOD\_RES 834 834  
 DR SITE 516 516  
 DR SITE 834 834  
 DR CARBOHYD 72 72  
 DR CARBOHYD 73 79  
 DR CARBOHYD 133 133  
 DR CARBOHYD 163 163

FT CARBOHYD 203 203 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 218 218 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 267 267 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 375 375 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 402 410 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARSPIC 529 612 MISSING (IN ISOFORM D).  
 FT VARSPIC 613 839 YVOIKRDIYAKRELGEAFKVFIAECYNISPTKMLV  
 FT VARSPIC 712 725 AVKALDKPTLAKDFORAEELTNQHEHYKFGVCGD  
 FT CONFLICT 70 70 DP -> WPSINDNGIILKDNROHLYSTHYIEEPVO  
 FT CONFLICT 635 635 SCEVSPRSGHGREIMNIPISLPGHSKPLNHIYEDVAVY  
 FT CONFLICT 635 635 ESKGRGE (IN ISOFORM B).  
 FT CONFLICT 635 635 MISSING (IN ISOFORM B).  
 FT CONFLICT 635 635 N -> S (IN REF. 2).  
 FT CONFLICT 635 635 D -> N (IN REF. 2).  
 SQ SEQUENCE 839 AA; 94455 MW; 86D965A5003BADDD CRC64;  
 Query Match 17.3%; Score 792.5; DB 1; Length 839;  
 Best Local Similarity 25.9%; Pred. No. 1.6e-45;  
 Matches 254; Conservative 125; Mismatches 244; Indels 357; Gaps 38;  
 QY 6 NIPLVHI-----LTIVAFGSTKTL-----PKAIPITPLEYVDALVEE 43  
 DB 79 NITSHIEWRSRLIHTANADVMELYTGLOKLTITKNSLSRIOPAFKKNPRLHYRILNLSNR 138  
 QY 44 VAFMCVAVESYPOPEISWTRNKILIKLPDTRYSIRENGOLTLITLSEYD----- 91  
 DB 139 LTT-----LSW-----QLFOT-LSLR-----LQLEQNFNCSDIRKM 171  
 QY 92-----SDGTYCCTANNNGCA-----VESCGALQVYMKRITRPPINVKI 132  
 DB 172 QLMQEGEAKLSQNLXCINAD-----GSQLPFRMNISOCDL-----PEISVSHNLTV 221  
 QY 133 IGLKAVLPCTTMGNPKPFSVMT-----KQDSPRENSRIAVESGSLRIHNQKEAG-Q 187  
 DB 222 REGDNNAVITCNGSGSLPVDVMTVIGLQISINHTQNLNNTVNAIALTLVNTVTSSENGFT 281  
 QY 188 YRCVAKNSLG-----TAY-----SKVYKLEFEVAFILRAPE-----SHNYTFGSFVTLHCT 234  
 DB 282 LNCIAENNVGMNASVALTVYVPRVVSLE-----EPRLREHCLIEF-----V 324  
 QY 235 ATGIPVPTTWIENGNAVSSGS--QESVKDRYIDSLDLFTTKP-----GLYTCLATNK 287  
 DB 325 VGNRPPTLHMLHNGQLRESKIIHVEYVQEEISEGCLLF-NKPRHYNNNGVTLTAKNP 383  
 QY 288 HGEKSTAKAATTSIAEWSKPOKDNKGCAQYRGECNAVALAKDALVFLNITSYADPEEA 347  
 DB 384 LG-----TANQTIN-----GH-----FLKEPF--PEST 404  
 QY 348 QELVHTANNEIKVSVPCRAEALLCNHIFQESPGVPPPIPIGRCYCLAVKELFGA 407  
 DB 405 DNF1-----LDEVP----- 415  
 QY 408 KEMLVMEKTHRGILYRSEMHLLSVPRCKSLPRMHDPTACARLPHDYKNELKTPRMT 467  
 DB 416-----TPPT 420  
 QY 468 -SSKPSVDIPNLSSSSSSFSVSPYMTVIISMSFAIFLTLTTLLYCCRRKQWKN 526  
 DB 421 VTHKRED-----TFGVSAVGLAFAVLVLVLFVLMNKGRSKRFGM 464  
 QY 527 K-----KRESAAYTL-----TILPSLLDLRLHPNM-----YQRMPLNPKLISLEY 570  
 DB 465 KGPVAVISGEEDSASPLHINHIGITPSSL--DAGPDTVVVICMTRIPVIEINPOYFROGH 521  
 QY 571-----PRNIEIVRDIGGAGFGRVQOARGLLPEYPTMVAVKLKEBASD 618  
 DB 522 NCHKPDYVQHIKRDIVLAKRELGBAGFKVLAECYNISPTKDKMLVAVALKDKPTLA- 580

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QY 619 MOADFOREALMAEFDPNIVKILGVCAGKPMCLFEYMAVYDNLNEFLRSMSPHTVCSL 678
   | | | | | : : : | | | : : | | | : | | | | | : | | | : |
Db 581 ARKFOREAEELITMLQHEHIVKFGVCGDGPLMLVEFMHSGDLNFKRAGHD----- 635
QY 679 SHSDLSMRAQVSSPP-----PLSCAEQLCIAROVAAGMAVLSERKRVHDLATRNCLV 733
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 636 -----AMILVGOFRQAKGELGSLQMLHIASQIASGMVYLASQHFHBDLATRNCLV 687
QY 734 GENNVYKADGCLSRNIYSADYK-----ANEND-----ALPRMPPESIFNRY 779
   | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 688 GANLVKIGDGMGRDVISTDYRLFNPSGNDPCICEVGGHTMLPRKMPESIMTRKF 747
QY 780 TTESDVAVGVVLEIFSYGLPPYGAHAEVYIYVRDGNILSCPENCPVELYMLRLCW 839
   | | | | | : | | | | | : | | | : | | | : | | | : | | |
Db 748 TTESDVAVSGVILWEIFTYGKQPMFQSLNTEVICITGGRVLERPRCPKEVYVLMGCM 807
QY 840 SKLPADRPSTSHIRLERM 859
   | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 808 QREPOQRILNKEIKILHAL 827

RESULT 13
TRKC_PIG STANDARD; PRT; 825 AA.
ID TRKC_PIG
AC P24786;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NT-3 growth factor receptor precursor (EC 2.7.1.112) (TrkC tyrosine
  kinase) (GP145-TrkC) (Trk-C).
GN NTRK3 OR TRKC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_Taxid=9623;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91364178; PubMed=1653651;
RA Lamballe F., Klein R., Barbacid M.;
RT "trkC, a new member of the trk family of tyrosine protein kinases, is
  a receptor for neurotrophin-3."
RL Cell 66:967-979(1991).
CC -1- FUNCTION: RECEPTOR FOR NEUROTROPHIN-3 (NT-3). THIS IS A TYROSINE-
  PROTEIN KINASE RECEPTOR. KNOWN SUBSTRATES FOR THE TRK RECEPTORS
  ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
  tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
  AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY IN THE BRAIN, LOW LEVELS IN THE
  OVARY.
CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
  PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M80800; AAA31130.1; -.
CC PIR: A40026; A40026.
CC HSSP: P11362; IFGK.
CC InterPro: IPR000719; Euk_Pkinase.
CC InterPro: IPR003599; Ig.

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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR002011; Receptor_tyr_kin_II.
DR InterPro: IPR001245; Tyr_Pkinase.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00560; LRR; 2.
DR Pfam: PF01463; LRRNT; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Tyrosine-protein kinase; Transmembrane; ATP-binding;
  phosphorylation; Receptor; Glycoprotein; Neurogenesis; Signal;
  leucine-rich repeat; Repeat; Immunoglobulin domain.
KW Leucine-rich repeat; Repeat; Immunoglobulin domain.
FT SIGNAL 1 31
FT CHAIN 1 825
FT DOMAIN 32 429
FT TRANSMEM 430 453
FT DOMAIN 454 825
FT REPEAT 102 125
FT REPEAT 126 149
FT REPEAT 227 288
FT DOMAIN 319 382
FT DOMAIN 538 814
FT NP_BIND 544 552
FT BINDING 572 572
FT ACT_SITE 679 679
FT MOD_RES 516 516
FT MOD_RES 705 705
FT MOD_RES 709 709
FT MOD_RES 710 710
FT MOD_RES 820 820
FT SITE 516 516
FT SITE 820 820
FT SITE 820 820
FT CARBOHYD 68 68
FT CARBOHYD 72 72
FT CARBOHYD 79 79
FT CARBOHYD 133 133
FT CARBOHYD 163 163
FT CARBOHYD 203 203
FT CARBOHYD 218 218
FT CARBOHYD 232 232
FT CARBOHYD 259 259
FT CARBOHYD 267 267
FT CARBOHYD 272 272
FT CARBOHYD 294 294
FT CARBOHYD 375 375
FT CARBOHYD 388 388
SO SEQUENCE 825 AA; 93129 MW; A3C6716B10D28540 CRC64;

Query Match 17.38; Score 788.5; DB 1; Length 825;
Best local Similarity 24.28; Pred. No. 2.9e-45;
Matches 234; Conservative 132; Mismatches 255; Indels 347; Gaps 27;

QY 6 NIPLVHT-----LTLVAFSGTEKL-----PKAPVITTPLETVDAVVEE 43
   | | | | | : : : | | | : | | | : | | | : | | | : |
Db 79 NITSHIENMRGLHTLNAVDELVTGLOKLTIKNSGLRSIOPRAFAKPHRIYINLSNR 138
QY 44 VATEFCAVESYPOPEISWTNRKILIKLFDTRYISRENGQLTLTISVED----- 91
   | | | | | : | | | : | | | : | | | : | | | : |
Db 139 LTT-----LSM-----QLFQT-LSLRE-----LRLEGNFNCSDIRMM 171

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OY 92 -----SDGIIYCCSTANNGVGA-----VESGALQVYKMKRTPPIINVY 132
DB 172 QLMQEGEAKLNGSLYCSAD-----GSOLPLFRMNIISQCDL-----PEISSHNLVY 221
OY 133 IEGKAVLFCCTTMGNPKPSVSMI-----KQDSPLENSRIAVLESGSLRHNVOKEDAG-Q 187
DB 222 REDNNAVVCNCGSPPLPVDMLVVTGLQSIINHQTNLMNTNVAIMLTLVNTSEONGFT 281
OY 188 YRCVAKNSGTAYSKV-VKLEFEVFARILRAPE---SHNVTEGSEFVTLCTATGIVPPI 243
DB 282 LUCIAENYVGMASVALVHPPRYVSLPEELREHCIEP-----VVRGNPPPL 333
OY 244 TWIENGNVSSGSIQESVADYDLSHQLPITKGLYCIATNKGKESTAKAATISI 303
DB 334 HMLHNG----- 339
OY 304 AEMSKQKQNKGYCAQREVCNAVLAADALVPLNTSYADPREAQLELHYTMANELKAVS 363
DB 340 ---QPLRSK-----ITHVEYQGEVS 359
OY 364 PVCRAEALLCNHIFQECSPGVVPTPICREYCLAVKELFCAKEMLVMEETHRGLYR 423
DB 360 EGC-----LLENKPTH----- 370
OY 424 SEMHLLSVKCKSLPMSHMDPTACARLPHLDYKNEN--LKTPEPMTSSKPSVD----- 474
DB 371 -----YNGNYTLNROPELGTANOTINGHFLKEP 399
OY 475 IYNLPSSSSSFVSPTSMTYI-----ISIMSFALPVLITLTYCCRRKKQK 525
DB 400 PESTDNEVSYFEVPTPTTYTHKEDEPTFGVSIAGLAACVLLVLFIMINKYGR 459
OY 526 NKRRESAATLTTLPSSELLDLRLHPMYO-----RMPLLNPKLISL 568
DB 460 SFGKMGPAVAISGEEDSAPLHNDOPMHHNLTIGRAGHSVIGMTRIPVLENPOYFQ 519
OY 569 EY-----PRNNIEYVRDIEGAFRGVFGARAGDGLLYEPFTVAVAKMLEAS 616
DB 520 GNCHCKPDTYVOHIKRRDYLKRELEGEAFGVFLAECYNLSPTKYKMLVAVVALLDPTL 579
OY 617 ADMQADFOREALMAFEDNPNTIKLGVCAVCKPMCLFREYAAVYDGLNEFRMSHPYVC 676
DB 580 A-ARQDFQEAELITNLMQENHYKFGVCGDDPLTWVEIKHGDNLKFLRHNGD--- 635
OY 677 SLSHSDLSMRAQVSSPPGP-----PLSCAEQLCIARQAVAGNAVYLSERKFEVHDLATRNC 731
DB 636 -----AMILVDCGRQAKGELGSLQMLHIASQISGVYLASQHFVHRDLATRNC 685
OY 732 LVGENNVKIALDFGLSRNITYSADYKANKENDALPIRMMPESIFRYKRTTESDYNAVYV 791
DB 686 LVGANLTVIKIGFGMSRDYSTDYRVFGHTMLPIRMMPESIMYKRTTESDYVMSFGYI 745
OY 792 LWEIFSYGLQPYGMANHEEVIYVVRGNTLSCPENCPELVYINMLRCLMSKLPADRSPTS 851
DB 746 LWEIFSYGQPMFQLSNTEVIECTIOGRVLERPRVCCKEYIVDMGLCMQREPORLNIKE 805
OY 852 IHRILERM 859
DB 806 IYKILHAL 813

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RESULT 14
TRKA_RAT
ID TRKA_RAT STANDARD: PRT: 799 AA.
AC P35739:
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE High affinity nerve growth factor precursor (EC 2.7.1.112)
DE (p140-TrkA) (Slow nerve growth factor precursor) (Trk-A).
GN NTRK1 OR TRKA OR TRK.
OS Rattus norvegicus (Rat).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RX SEQUENCE FROM N.A. (TRKA-II ISOFORM).
RX MEDLINE=92196121; PubMed=1312719;
RT Weakin S.O., Suter U., Drinkwater C.C., Welcher A.A., Shooter E.M.;
RT "The rat trk protooncogene product exhibits properties characteristic
RT of the slow nerve growth factor receptor.";
RT Proc. Natl. Acad. Sci. U.S.A. 89:2374-2378(1992).
RN [2]
RN ALTERNATIVE SPLICING.
RX MEDLINE=93315496; PubMed=8325889;
RA Barker P.A., Lomen-Hoerth C., Gensch E.M., Weakin S.O., Glass D.J.,
RA Shooter E.M.;
RT "Tissue-specific alternative splicing generates two isoforms of the
RT trkA receptor.";
RT J. Biol. Chem. 268:15150-15157(1993).
CC -1- FUNCTION: REQUIRED FOR HIGH-AFFINITY BINDING TO NERVE GROWTH
CC FACTOR (NGF), NEUROTROPHIN-3 AND NEUROTROPHIN-4/5 BUT NOT BRAIN-
CC DERIVED NEUROTROPHIC FACTOR (BDNF). KNOWN SUBSTRATES FOR THE TRK
CC RECEPTORS ARE SHC, PI-3 KINASE, AND PLC-GAMMA-1. HAS A CRUCIAL
CC ROLE IN THE DEVELOPMENT AND FUNCTION OF THE NOCICEPTIVE RECEPTION
CC SYSTEM AS WELL AS ESTABLISHMENT OF THERMAL REGULATION VIA
CC SWEATING. ACTIVATES ERK1 BY EITHER SHC- OR PLC-GAMMA-1-DEPENDENT
CC SIGNALING PATHWAY (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -> ADP + protein
CC tyrosine phosphate.
CC -1- SUBUNIT: EXISTS IN A DYNAMIC EQUILIBRIUM BETWEEN MONOMERIC (LOW
CC AFFINITY) AND DIMERIC (HIGH AFFINITY) STRUCTURES.
CC -1- SUBCELLULAR LOCATION: type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; TRKA-I AND TRKA-II (SHOWN
CC HERE); ARE PRODUCED BY ALTERNATIVE SPLICING. BOTH ISOFORMS HAVE
CC SIMILAR BIOLOGICAL PROPERTIES.
CC -1- TISSUE SPECIFICITY: TRKA-II IS PRIMARILY EXPRESSED IN NEURONAL
CC CELLS; TRKA-I IS FOUND IN NON-NEURONAL TISSUES.
CC -1- PTM: LIGAND-MEDIATED AUTO-PHOSPHORYLATION.
CC -1- SIMILARITY: BELONGS TO THE INSULIN RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES. TRK-TYPE SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 LEUCINE-RICH REPEATS (LRR).
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-----
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CC EMBL: M85214; AAA42286.1; -
CC EMBL: L12225; -; NOT_ANNOTATED_CDS.
CC PIR: A41981; TVRTTB.
CC HSP: P11362; IFCG.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR003599; Ig.
CC InterPro: IPR001611; LRR.
CC InterPro: IPR000483; LRR_Cterm.
CC InterPro: IPR002011; Receptor_tyr_kin_II.
CC InterPro: IPR001245; Tyr_pkinase.
CC Pfam: PF00560; LRR_2.
CC Pfam: PF00069; pkinase_1.
CC PRINTS: PR00109; TYRKINASE.
CC SMART: SM00409; IG_1.
CC SMART: SM00082; LRRCD_1.
CC SMART: SM00219; TYRK_1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
CC PROSITE: PS00109; PROTEIN_KINASE_TYR_1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
CC PROSITE: PS00239; RECEPTOR_TYR_KIN_II_1.
CC Transferrase: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
CC Leucine-rich repeat; Immunoglobulin domain; Neurogenesis;

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DR EMBL: U3635; AAA87565.1; -  
 DR EMBL: U40271; AAC50484.1; -  
 DR HSP: P12931; 1FMK.  
 DR MIM: 601890; -  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003588; Ig\_C2.  
 DR InterPro: IPR003600; Ig\_Like.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00047; Ig; 7.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR SMART: SM00410; IG\_Like; 2.  
 DR SMART: SM00408; IGC2; 5.  
 DR SMART: SM00219; Tyrc; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW Receptor; Transmembrane; Signal; Glycoprotein; Cell adhesion;  
 KW Immunoglobulin domain; Repeat.  
 FT SIGNAL 1 30  
 FT CHAIN 1 1070  
 FT TRANSIN 31 704  
 FT TRANSIN 705 725  
 FT DOMAIN 726 1070  
 FT DOMAIN 46 108  
 FT DOMAIN 143 208  
 FT DOMAIN 239 308  
 FT DOMAIN 336 398  
 FT DOMAIN 426 488  
 FT DOMAIN 517 577  
 FT DOMAIN 606 671  
 FT DOMAIN 796 1066  
 FT DISULFID 53 101  
 FT DISULFID 150 200  
 FT DISULFID 246 301  
 FT DISULFID 343 391  
 FT DISULFID 433 481  
 FT DISULFID 524 570  
 FT DISULFID 613 664  
 FT CARBOHYD 116 116  
 FT CARBOHYD 175 175  
 FT CARBOHYD 184 184  
 FT CARBOHYD 214 214  
 FT CARBOHYD 268 268  
 FT CARBOHYD 283 283  
 FT CARBOHYD 405 405  
 FT CARBOHYD 463 463  
 FT CARBOHYD 567 567  
 FT CARBOHYD 646 646  
 FT CONFLICT 92 92  
 FT CONFLICT 147 147  
 FT CONFLICT 207 207  
 FT CONFLICT 495 496  
 FT CONFLICT 515 515  
 FT CONFLICT 834 834  
 FT CONFLICT 881 881  
 FT CONFLICT 969 969  
 FT CONFLICT 992 992  
 SO SEQUENCE 1070 AA: 118260 MM: 47CDF25B8E3698A5 CRC64;

Query Match 16.9%; Score 774; DB 1; Length 1070;  
 Best Local Similarity 27.2%; Pred. No. 3.9e-44;  
 Matches 228; Conservative 137; Mismatches 304; Indels 168; Gaps 29;

55 POPFISWTRKILIKLFDTRKSTRENGQLLTISVEDSGIYCTTANNGVGAIVESGCA 114

Db 350 PERSVMEHAGVRL---PHGRVYQGHLEVLAMIAESDAGVYTCNANLAGORODVN- 405  
 QY 115 LQYKMKPTTRPPINVKIIEGLKAVLPCTTMGPKPSVSIKGDSPLENSRIAYLES 174  
 Db 406 IYATVPMSLKKRQDSQLEBGRKGYLDCLQATPKFTVYVRYOMLISDSRFEVKNKG 465  
 QY 175 LRTHNQKEDAGQRCVANKSLGTAISKYVKEFEVFAIRLAP---ESHNTFGSEVTL 231  
 Db 466 LRINSVEYDGTWYRCMSTPAGSIEAQAV---LQVLEKLFKPPPOQCMGFDEKAV 522  
 QY 232 HCTATGIPVPTITWINGNANVSGSIQESVKDRVIDSRQLQFLTK-----PGLYTIAIN 286  
 Db 523 PCSATGREKPTIKMER-----ADGS---SLPEVYDINAQTLHFAVTRDADAGNYCTIASN 574  
 QY 287 KIGEKFSTAKAATATSIASWSPKQDKNGYCAQYRGECNAVLAKDALFNTSYADPEE 346  
 Db 575 -----GPGQGIKRAHVQLVY---ANFI--TFKVEPR 600  
 QY 347 AQELLVHTAMNELKVSPVCRPAEALLCNHIFQESPGVVPPLPICREYCLAVKEFC 406  
 Db 601 TTVYQGHIA-----LLOCEAOGDKPL----- 622  
 QY 407 AKEMLVMEKTRHGLYRSEMHLISVPKSKLPSM-----WDPTACARLPHLDY 455  
 Db 623 -IQW-----KQDRILDPKLG-PRMHIFQGSVIYHDVAPEDSGRTTCIAG 667  
 QY 456 AKENIK-TFPPMTSSKPSVDIPLDSSSSSFSVSPYSM--TVIISWSPFAIVLTI 512  
 Db 668 NSCNKHTHEAPLY---VYDKP-VPESEGPQS-PPYKMIQTIGLSGAAVAIVAVLG 721  
 QY 513 TLYC---CRRKQKNNKRRSAVTL-----TTLPSELLDLRHPNMYQM 557  
 Db 722 LMFYKRRKCKAKRLOKQEBGEPEMECLNGRPLONGQPSAEIOEBVALTSGSGPAATNK 781  
 QY 558 PLLNPKLLSEYPPNNIEYVADIGEGAFGRVFOARGLPYEPFTWAVAKLKEASA 617  
 Db 782 RHSTSDK---MHFPSSLIQPTITLTKSEGEVFLAKAGLEGVAETLVIVKSLQSK-DE 837  
 QY 618 DMQADFOREALMAFEDNPNTVILGVCAGVRPKCLFEYNAYGDLNEFLMSMSPHYCS 677  
 Db 838 QOQDLFRRELEFGKLNANAVRRLGLCREAPHYVLEVYDLBKQFLR----- 888  
 QY 678 LSHS-DLSMAQVSSPPPLSCAEOLCIARQVAAAGMAYLSERKPHVDLATRNCLVNS 736  
 Db 889 ISKSKDEKLKQO-----PLSTQKVALCTQVALGHEHLSNNRPHVDLARNCLVSAQ 941  
 QY 737 MVYIADRGSLRNITYSADYKANENDALPIKMPPEISFYNRYTSDVMAVGVLMET 796  
 Db 942 ROVAVSALGSLSKDYVNSEYHFRQ-AWVALRMSPEALLEGDFSTKSDVMAVGVLMET 1000  
 QY 797 SYGLQPYVGMHEEVIYVYRDGNI-LSCPEMCPVELYNLMCLWSKLPADRPSTSI 852  
 Db 1001 THGEMPHQGDADDEVLDLQAGKARLPQEGCPSKLYRLMQRCVALSPKDRPSEI 1057

Search completed: August 16, 2002, 13:37:06  
 Job time: 66 sec



CC method uses a mutated PKR nucleic acid which comprises a modification to the intracellular and extracellular domains, or comprises a modification to the intracellular domain and excludes any nerve growth factor receptor(s) (NGFR). The method uses mutated PKR as a cell surface marker, and is useful for identifying genetically modified cells, especially immunoselection of transduced mammalian cells, and for identifying mammalian cells expressing a protein of interest. The genetically modified marked cells may be used in an autologous or allogeneic setting e.g. gene therapy for bone marrow transplants, graft facilitation or immune reconstitution.

CC Sequence 869 AA:

Query Match 100.0%; Score 4569; DB 22; Length 869;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 869; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MRELVIPIVHILTLVAFSGTEKLPKAPVITTPLETVDAIVEEATFMCAVESYPOPEIS 60  
1 mrelvnpilvhltilvafsgteklpkapvittpletvdalveeatfmcavesyppeis 60  
61 WTRNKILIKLFDRIYSIRENGQLTLISVEDSDGIYCTANNGVGVAVESGALGVKMK 120  
61 wtrnkililkfdrisirengqltlisvedsdgiyctanngvgvavescgalgvkmk 120  
121 PRTTRPPINWKIEGLKVLPCPTMGNPSPVSWIKGSDPLRENSRIAVLESGLRIHNV 180  
121 prttrppinwkiegkvlpcptmgnpvspvswikgdsplrensrivalesgslrihmv 180  
181 QKEDAGQYRCVAKNSIGTAYKYVKEFEVFAIRLAPESHNVTEGSEFVTLCHTATGIPV 240  
181 qkedagqyrcvaknsigtaykyvkefevfarilrapeshnvtegesefvtlchtatgipv 240  
241 PRTTWEENGNAVSSGSIQSVKDRITDSRLQFIRKPGIYTCIATYKHEKSTAKAAAT 300  
241 prttywengnavssgsiqsvkdrirtsrlqfirkpigiyciatykhkstkakaat 300  
301 ISIAEMSKPQKDKYCAQYRGEVCNANAKDALVFLNTSYADPEAOELVHTAMNELK 360  
301 isiaemskpqdkdkycayrgevcnanaakdalvflntsyadpeaoelvhtamnelk 360  
361 VVSPFCRAAEALLCNHIFQECSPGVVPTPTICREYCLAVELFCAKEMLVMEETKRG 420  
361 vvspfcraaeallcnhifqecspgvvptpticreyclavelfcakemlvmeetkrg 420  
421 LYRSEMHLSYPKCKLSMHMDPACARLPLDINKELTKFPFMTSSKPSVDIPNIPS 480  
421 lyrsemhlisypckcklsmhmdpacarlpldynkelkfpfmtsskpsvdipnips 480  
481 SSSSFSVSPYTSMTVIISINSSFAIFVLTITTYCCRRKQKMKKRESAAVLTLP 540  
481 ssssfsvspytsmtviisinsfaiFVLTITTYCCRRKQKMKKRESAAVLTLP 540  
541 SELLDLRHPMPQORMLLNPKILSEYPRNNIERYVDIGEGFVGFQARAPGLPY 600  
541 sellldlrhpmqormllnplkilsEYPRNNIERYVDIGEGFVGFQARAPGLPY 600  
601 EPTTVAVKMLKEBASADMDQDFORALMAEFDNPVTKLVGNCKKPKCLFEVAY 660  
601 epttvavkmlkebasadmdqdforalmAEFDNPVTKLVGNCKKPKCLFEVAY 660  
661 GDLNEFLRSMSPHTVCSLSHSDLSMRAOVSSPPPLSCAQLCLAROVAAGMAYLSRK 720  
661 gdlneflrsmshphtvcslsHSDLSMRAOVSSPPPLSCAQLCLAROVAAGMAYLSRK 720  
721 FVHEDLATRNLVGENNVKATADGLSRNITSADYKANENDAIPIRMPPESIFXNYT 780  
721 fvhdlatrnlvgennvkAtadglSRNITSADYKANENDAIPIRMPPESIFXNYT 780  
781 TESDVAAYGVVLAIEFSXGLOPYGMAHEEIVYVRDGNITSCBNCPVELYNMLCWS 840  
781 tesdvaaygvvLAIEFSXGLOPYGMAHEEIVYVRDGNITSCBNCPVELYNMLCWS 840  
841 TEEDVAYGVVLAIEFSXGLOPYGMAHEEIVYVRDGNITSCBNCPVELYNMLCWS 840  
841 teedvaygvvLAIEFSXGLOPYGMAHEEIVYVRDGNITSCBNCPVELYNMLCWS 840

DB 841 KIPADPSTSHRIIRNCEERAGTVSV 869  
841 kipadpstsHRIIRNCEERAGTVSV 869

RESULT 3  
ID AAM26611 standard; Protein; 869 AA.  
AAM26611;  
27-JAN-1998 (first entry)

Human muscle-specific kinase (Musk).  
Receptor tyrosine kinase; muscle specific kinase; Musk; Dmk; human.  
ligand; agrin; diagnosis; therapy.

Hom sapiens.  
(M09721811-A2.

19-JUN-1997.

13-DEC-1996; 96MO-US20696.

10-MAY-1996; 96US-0644271.

15-DEC-1995; 95US-0008657.

(REG-) REGENERON PHARM INC.

Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD;

WPI, 1997-332783/30.

DR N-PSDB; AAT90473.

Nucleotide sequences encoding human agrin and muscle specific kinase and related receptor - used in diagnosis and treatment of disorder with muscle atrophy

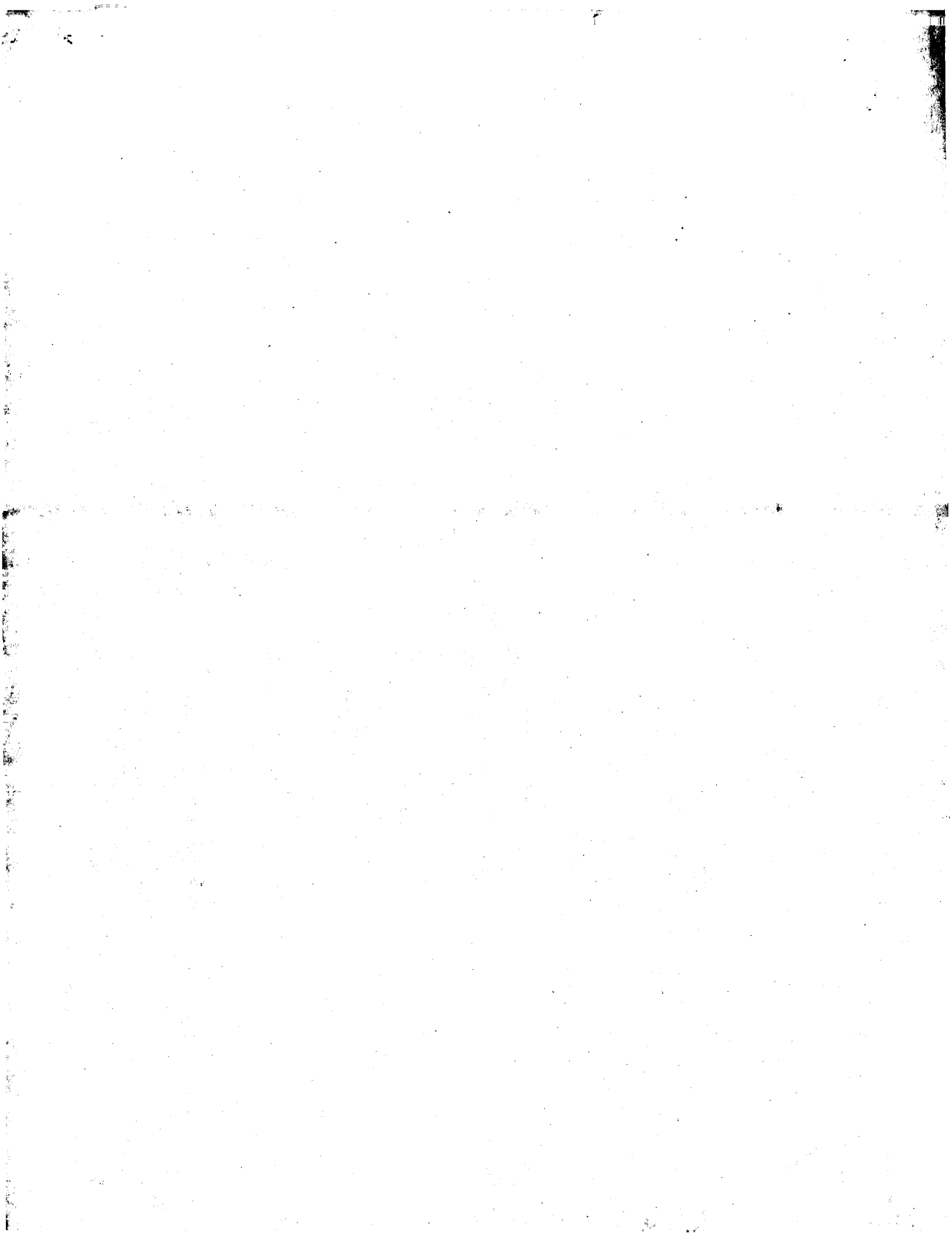
Example 4; Fig 4; 120pp; English.

This polypeptide comprise a novel human receptor tyrosine kinase designated muscle specific kinase (Musk) that is expressed in normal and denervated muscle. Musk is alternatively referred to Dmk for denervated muscle kinase. The amino acid sequence was deduced from an isolated cDNA clone (see AAT90471). Rat Musk (see AAM26610) has also been identified. Use of Musk to generate anti-Musk antibodies and in the diagnosis of neurological or other disorders is disclosed. Assay systems that may be used to detect and/or measure ligands that bind the musk gene product are provided. A claimed method of promoting the growth, differentiation or survival of Musk receptor-expressing cells involves administration to the cell of agrin (see AAM26609). Such cells include muscle, heart, spleen, ovary and retina cells, or cells genetically engineered to express the Musk receptor.

Sequence 869 AA:

Query Match 99.8%; Score 4558; DB 18; Length 869;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 MRELVIPIVHILTLVAFSGTEKLPKAPVITTPLETVDAIVEEATFMCAVESYPOPEIS 60  
1 mrelvnpilvhltilvafsgteklpkapvittpletvdalveeatfmcavesyppeis 60  
61 WTRNKILIKLFDRIYSIRENGQLTLISVEDSDGIYCTANNGVGVAVESGALGVKMK 120  
61 wtrnkililkfdrisirengqltlisvedsdgiyctanngvgvavescgalgvkmk 120



```

OY 121 PKTRPPINVKIIEGLKAVLPCTMGNPKPSVSWIKGDSPLRENSRIAVLESGSLRINHV 180
Db 121 PKTRPPINVKIIEGLKAVLPCTMGNPKPSVSWIKGDSPLRENSRIAVLESGSLRINHV 180
OY 181 OKEDAGOVRCVAKNSLGTAISKVVKLEFEVFAIRILRAPESHNVTFGSEVTLHCTATGIPV 240
Db 181 OKEDAGOVRCVAKNSLGTAISKVVKLEFEVFAIRILRAPESHNVTFGSEVTLHCTATGIPV 240
OY 241 PTTWIENGNAVSSGSIQESVDRVIDSRLOLFTFKPELTYCIATNKGGEFSTAKAAAT 300
Db 241 PTTWIENGNAVSSGSIQESVDRVIDSRLOLFTFKPELTYCIATNKGGEFSTAKAAAT 300
OY 301 ISIAEWSKPOKDNKGYCAOYRGECVNAVLAKDALVFLNTSYADPEAOELLVHTANNEKX 360
Db 301 ISIAEWSKPOKDNKGYCAOYRGECVNAVLAKDALVFLNTSYADPEAOELLVHTANNEKX 360
OY 361 VVSPVCRPAEALLCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKEWLVMEKTHRG 420
Db 361 VVSPVCRPAEALLCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKEWLVMEKTHRG 420
OY 421 LYREEMHLISVPCSKLPSMMDPTACARPLHLDYNNKENTLTFPPMSSKSSVDIPNIPS 480
Db 421 LYREEMHLISVPCSKLPSMMDPTACARPLHLDYNNKENTLTFPPMSSKSSVDIPNIPS 480
OY 481 SSSSSFSVSPRTYSMTVTIISIMSSFAIVLTLTTLYCCRRRQKQKKNKRESAAVTLATLP 540
Db 481 SSSSSFSVSPRTYSMTVTIISIMSSFAIVLTLTTLYCCRRRQKQKKNKRESAAVTLATLP 540
OY 541 SELLDLRLHPMYORMBLLNPKLLSLFYRNNIEYVROJGEGAFGVFOARAPGLLPY 600
Db 541 SELLDLRLHPMYORMBLLNPKLLSLFYRNNIEYVROJGEGAFGVFOARAPGLLPY 600
OY 601 EPTTVAVKMLKEBASADMQDFOREALMAEFDPNPVILKLGCAVGRKPMCLTFEYMAX 660
Db 601 EPTTVAVKMLKEBASADMQDFOREALMAEFDPNPVILKLGCAVGRKPMCLTFEYMAX 660
OY 661 GDNIEPLRMSPRVYCSLSHSDLSMRQVSPGPPPLSCABOLCTIAROVAAGAAVLSERK 720
Db 661 GDNIEPLRMSPRVYCSLSHSDLSMRQVSPGPPPLSCABOLCTIAROVAAGAAVLSERK 720
OY 721 FVHRDLATRNCLVGENNVKVIADFGLSRNIYSADYKANENDAPIRMMPESIFYYRYT 780
Db 721 FVHRDLATRNCLVGENNVKVIADFGLSRNIYSADYKANENDAPIRMMPESIFYYRYT 780
OY 781 TESVNAVAYVVLMEISTYGLQPIYGAHHEVYTYVRDGNILSCPCNPVELLYNMLRCLWS 840
Db 781 TESVNAVAYVVLMEISTYGLQPIYGAHHEVYTYVRDGNILSCPCNPVELLYNMLRCLWS 840
OY 841 KLPADRPSTSIHRIILERMCRAGTYSV 869
Db 841 KLPADRPSTSIHRIILERMCRAGTYSV 869

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## RESULT 4

AAW26506  
ID AAW26506 standard; Protein; 869 AA.

AAW26506:

06-JAN-1998 (first entry)

Human Dmk receptor.

Dmk receptor; tyrosine kinase receptor; signal transduction; assay;

therapy; diagnosis; Alzheimer's disease; Parkinson's disease;

amyotrophic lateral sclerosis; Lou Gehrig's disease;

idiopathic torsion dystonia; muscle atrophy.

Homo sapiens.  
US5656473-A.  
12-AUG-1997.

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XX 21-JUL-1993: 9305-0095658.
PF 19-JAN-1995: 9505-0374834.
PR 21-JUL-1993: 9305-0095658.
PA (REG-) REGENERON PHARM INC.
XX Rojas EA, Valenzuela DM;
PI WPI: 1997-414593/38.
DR N-PSDB; AAT87073.
XX New isolated human denervated muscle kinase receptor - used to
PT develop products for the diagnosis and treatment of neurological,
PT muscle or neuromuscular disorders
PS Claim 4; Column 31-36; 31pp; English.
XX This polypeptide comprises the human Dmk receptor (AAW26506), a novel
CC tyrosine kinase receptor that is expressed in high levels in
CC denervated muscle. Its amino acid sequence was deduced from an
CC isolated nucleic acid molecule (see AAT87073). The Dmk receptor can
CC be used to screen for agents that interact with Dmk. Agents that
CC bind to the receptor may mediate survival and differentiation in
CC cells naturally expressing the receptor, but may also confer survival
CC and proliferation when used to treat cells engineered to express the
CC receptor. Dmk receptor polypeptides and polynucleotides can also be
CC used for detecting abnormalities in the function or expression of the
CC receptor which may be used in the diagnosis of muscular or other
CC disorders. Manipulation of the receptor or agonists which bind this
CC receptor may be used to treat neurological diseases, diseases of
CC muscle or neuromuscular unit disorders, including Alzheimer's
CC disease, Parkinson's disease, amyotrophic lateral sclerosis (Lou
CC Gehrig's disease), idiopathic torsion dystonia and muscle atrophy.
CC The extracellular domain (ECD) of the receptor can be used to block
CC the binding of receptor to target cells. A receptorbody comprising
CC the ECD fused to a human Ig gamma-1 constant region is claimed.
SO Sequence 869 AA:

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## Query Match

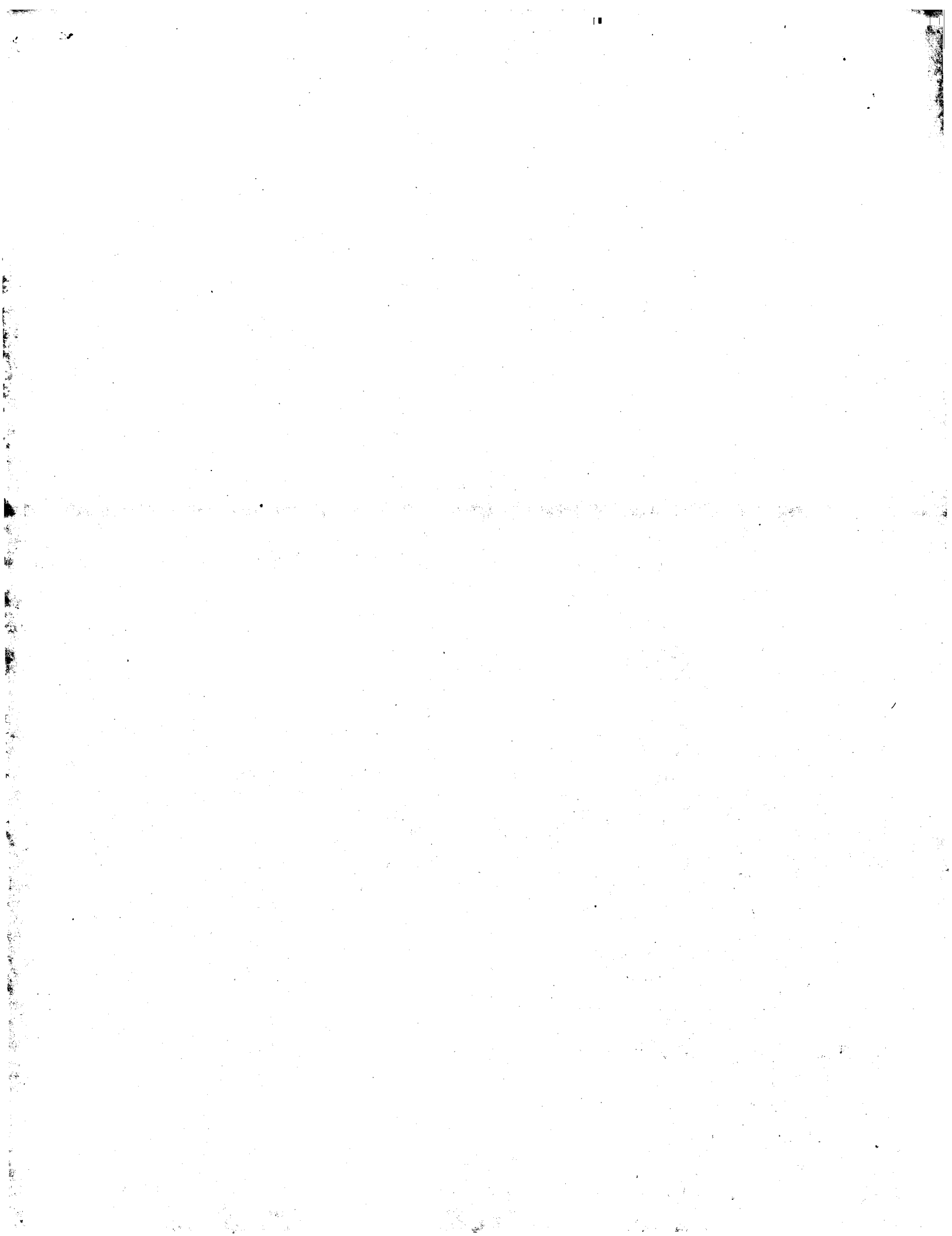
Best Local Similarity 99.8%; Score 4558; DB 18; Length 869;

Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MRLVNIPLVHILTLVAFSTETLPRAPVITTLLEVVDALVEEVAIFMCAVESEIPEIS 60
OY 61 WTRNKLILKLFDRYSIRENGOLLTITLSEVSDSDGTYCCGANNVGAVSSGALQYKMK 120
Db 61 WTRNKLILKLFDRYSIRENGOLLTITLSEVSDSDGTYCCGANNVGAVSSGALQYKMK 120
OY 121 PKTRPPINVKIIEGLKAVLPCTMGNPKPSVSWIKGDSPLRENSRIAVLESGSLRINHV 180
Db 121 PKTRPPINVKIIEGLKAVLPCTMGNPKPSVSWIKGDSPLRENSRIAVLESGSLRINHV 180
OY 181 OKEDAGOVRCVAKNSLGTAISKVVKLEFEVFAIRILRAPESHNVTFGSEVTLHCTATGIPV 240
Db 181 OKEDAGOVRCVAKNSLGTAISKVVKLEFEVFAIRILRAPESHNVTFGSEVTLHCTATGIPV 240
OY 241 PTTWIENGNAVSSGSIQESVDRVIDSRLOLFTFKPELTYCIATNKGGEFSTAKAAAT 300
Db 241 PTTWIENGNAVSSGSIQESVDRVIDSRLOLFTFKPELTYCIATNKGGEFSTAKAAAT 300
OY 301 ISIAEWSKPOKDNKGYCAOYRGECVNAVLAKDALVFLNTSYADPEAOELLVHTANNEKX 360
Db 301 ISIAEWSKPOKDNKGYCAOYRGECVNAVLAKDALVFLNTSYADPEAOELLVHTANNEKX 360
OY 361 VVSPVCRPAEALLCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKEWLVMEKTHRG 420
Db 361 VVSPVCRPAEALLCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKEWLVMEKTHRG 420

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OY 421 LYRSEMHLLSVKCKSLPSMHDPTACARLPHLDYKNENLKTPEPMTSKSPVDIPNLS 480
DB 421 lysemhllsvpeckslpsmhdptacarlphldynkenlktfpmtskspvdipnls 480
OY 481 SSSSFSVSPYSMYIISIMSSFAIFVLLITTLCCRRRQWKKKRESAAVTLTLTP 540
DB 481 ssssfsvspysmyiisimssfaifvllitlccrrrkqwkkrresaavtltltp 540
OY 541 SELLDRLHPNMYQRMPLLNPKLISLEYPRNNIEYRDIGEGAFGVQARAPGLLPY 600
DB 541 sellldrlhpnmyqrmpllnpkllisleypnnieyrvdigegafgvqarapgllyp 600
OY 601 EPTTMAVVKMLKEASADMQADFOREALMAEFDPNINIVKLIGVCAVGKPMCLLFEYMA 660
DB 601 epttmavvkmleasadmoadforealmaefdpninvkligvcavgkpmcllfeymay 660
OY 661 GDLMELFRSKSPHYVCSHSDLSMKRAOVSSPPPEPLSCAQLCTAROVAAGMAYLSERK 720
DB 661 gdlmelfrsksphyvcsishdlsmkraovsspppeplscaqcltarovaagmaylsesk 720
OY 721 FVHDLATRNCLVGENMYKTADEGLSNIRYSADYKANKENDAIPIRMPESTIFYNRYT 780
DB 721 fvhdlatrnclvgenmyktaadeglsnirysadykankendaipirmpestifynryt 780
OY 781 TESQVMAVGVVLMETFSYGLQPIYGMAREEVIYVRDGNILSCPEVPELYNLMRLQWS 840
DB 781 tesqvavgvvlmetfsyglqpiygmareeviyvrdgnilscpevpelynlmrlqws 840
OY 841 KLPAIDRPSFMSIHRILERMCRACGYSV 869
DB 841 klpaidrpsfshrlermcraegvsv 869

RESULT 5
ID AAM26610 standard; Protein: 868 AA.
AC AAM26610:
XX 27-JAN-1998 (first entry)
DE Rat muscle-specific kinase (Musk).
KW Receptor tyrosine kinase; muscle specific kinase; Musk; Dmk; rat;
XX ligand; agrin; diagnosis; therapy.
XX Rattus sp.
FH Key Location/Qualifiers
FT Peptide 1..19
FT Domain /label= sig_peptide
FT Domain /label= Extracellular_domain
FT Domain 493..521
FT /label= Transmembrane_domain
FT Domain 522..868
FT /label= Intracellular_domain

MO9721811-A2.
XX 19-JUN-1997.
XX 13-DEC-1996: 96MO-0520696.
XX 10-MAY-1996: 96US-0644371.
XX 15-DEC-1995: 95US-0008657.
XX (REG-) REGENERON PHARM INC.
XX Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD:
XX WPI, 1997-332783/30.

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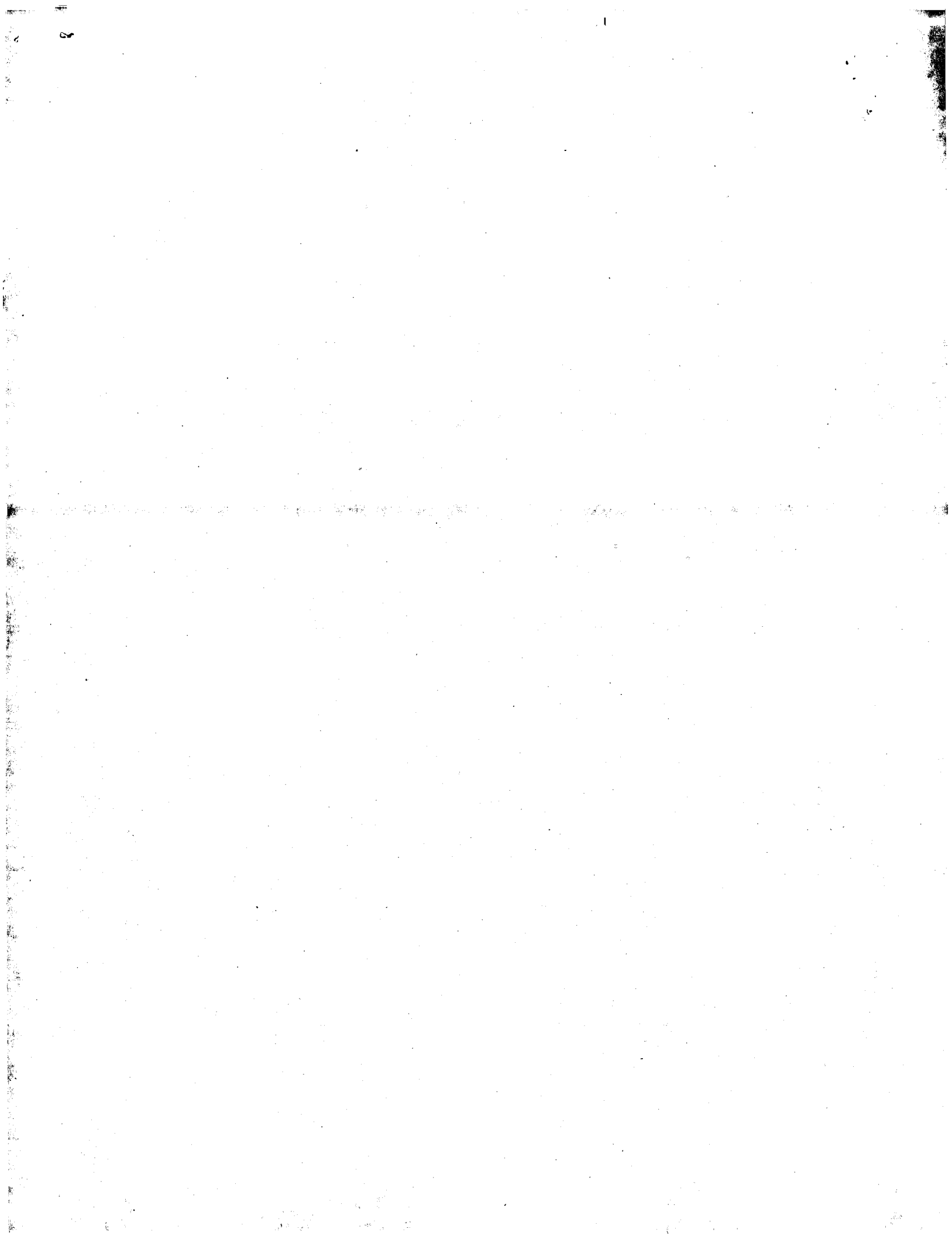
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DR N-PSDB: AAT90472.
XX Nucleotide sequences encoding human agrin and muscle specific kinase
PT and related receptor - used in diagnosis and treatment of disorder
PT with muscle atrophy
XX
PS Example 1; Fig 1; 120pp; English.
XX
CC This polypeptide comprise a novel rat receptor tyrosine kinase
CC designated muscle specific kinase (Musk) that is expressed in
CC normal and denervated muscle. Musk is alternatively referred to
CC Dmk for denervated muscle kinase. The amino acid sequence was
CC deduced from an isolated cDNA clone (see AAT90472). Human Musk (see
CC AAM26611) has also been identified. Use of Musk to generate anti-
CC Musk antibodies and in the diagnosis of neurological or other
CC disorders is disclosed. Assay systems that may be used to detect
CC and/or measure ligands that bind the musk gene product are provided.
CC A claimed method of promoting the growth, differentiation or
CC survival of Musk receptor-expressing cells involves administration
CC to the cell of agrin (see AAM26609). Such cells include muscle,
CC heart, spleen, ovary and retina cells, or cells genetically
CC engineered to express the Musk receptor.
XX
SQ Sequence 868 AA:

Query Match 93.9%; Score 4292.5; DB 18; Length 868.
Best Local Similarity 93.2%; Pred. No. 0;
Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

OY 1 MRELVINPIVLHITLVAFSCTEKLKRAVITTPLETVDALVEEVAFTPMCAVESYPOEIS 60
DB 1 mrelnvnpilqmltlvaifscteklkrapvltpletvdalveevatlmcavesypoeis 60
OY 61 WTRNKILIKLFDTRYISIRENGQLITLLSVEDSDGICYCTANNVGAVESGALQYKMK 120
DB 61 wtrnkliklfdtryisirengqlitllsvedsdgylycctannvgavescgalqykkm 120
OY 121 PKITRPINVKIIEGLKAVLPCTMGNPKPSVMIKGDSPLENSKRAVLESGLRIHNV 180
DB 121 pkltrpinvkiieglkavlpctmgnpkpsvmiikgdsplenskraavlsgslrihny 180
OY 181 QKEDAGQRCVAAKNSLTATSKYVKLEFEVFAILRLAPESHNVTGSEFVLHCGATGIPV 240
DB 181 qkedagqrcvvaaknsltatksyvklefevfaillrlapeshnvtgsefvllhcgatgipv 240
OY 241 PTTTWIENGNAVSSGSIQESVKDVIDSRQLPFTTRPGLYTCIATNKGKFEFTAKAAAT 300
DB 241 pttwiengnavssgsioesvkdrvidsrqlpfttrpglytciatnkgkfeftakaaat 300
OY 301 ISIAEMSKPOKDKNGYCAQYRGECVNAVLAKDALVFLNTSYADPEEKOELLVHTANNEK 360
DB 301 isiaemskpokdkngycayrgecvnavlakdalvflntsyadpeekeollvhtannek 360
OY 361 VSLAEWSKSKESKQYCAQYRGECDAVLKDSLVFTNSYDPEEQELLHITLAVNELK 360
DB 361 vslaewskskeskqycaqyrgecdavlvkdslvftnsydpееqellhitlavelnk 360
OY 421 VSPVCRPAEALLCNHIFQECSPGVVPTPIPCREYCLAVKELFCAKELVAEKEKTHRG 420
DB 421 vspvcrpaallcnhifqecspgvvptpipcreyclavkelcfaekelvaeekthrg 420
OY 421 LYRSEMHLLSVKCKSLPSMHDPTACARLPHLDYKNENLKTPEPMTSKSPVDIPNLS 480
DB 421 lysemhllsvpeckslpsmhdptacarlphldynkenlktfpmtskspvdipnls 480
OY 481 SSSSFSVSPYSMYIISIMSSFAIFVLLITTLCCRRRQWKKKRESAAVTLTLTP 540
DB 481 ssssfsvspysmyiisimssfaifvllitlccrrrkqwkkrresaavtltltp 540
OY 541 SELLDRLHPNMYQRMPLLNPKLISLEYPRNNIEYRDIGEGAFGVQARAPGLLPY 600
DB 541 sellldrlhpnmyqrmpllnpkllisleypnnieyrvdigegafgvqarapgllyp 600
OY 601 EPTTMAVVKMLKEASADMQADFOREALMAEFDPNINIVKLIGVCAVGKPMCLLFEYMA 660
DB 601 epttmavvkmleasadmoadforealmaefdpninvkligvcavgkpmcllfeymay 660

```



QY 661 GDINEFLRSMSPHTVCSLSHSDLSMRAOVSSPPGPLSCAEOLCIARQVAAAGMAYLSERK 720  
 Db 660 gdineflrsmshphtvcslshsdlsrtravspgppplscaeqlclarqvaagmaylsertk 719  
 QY 721 FVHRDLATRNCLVGENMVKVITADFGLSRNIYSADYRKANENDAIPIRMMPPESTFYNNRT 780  
 Db 720 fvhrlatrnclvgenmvkltadfglsrnllysadylkaadgnadaiplrmppestlfnrlyt 779  
 QY 781 TESDVWAVGVVLMWEIFSYGLQPYTGMAHEEVIYVRDGNILSCPENCPVELYNMLRLCWS 840  
 Db 780 tesdvwavgvvlmwelfsyglqpytgmaheevlyyvrdsnllacpencpvelynmlrlcws 839  
 QY 841 KLPA DRPSTSHRIIRLIERMCEERAGTYSV 869  
 Db 840 klpadrpfstshrlirmceragetyv 868

## RESULT 6

AAW26507  
 AAW26507 standard; Protein: 868 AA.

AAW26507;

06-JAN-1998 (first entry)

Rat Dmk receptor.

Dmk receptor; tyrosine kinase receptor; signal transduction; assay; therapy; diagnosis.

Rattus sp.

Key Location/Qualifiers

Peptide 1..19

Domain 20..492

Domain 492..521

Domain 522..868

Domain 869..868

Domain 869..868

Domain 869..868

Domain 869..868

Domain 869..868

Domain 869..868

Domain 869..868

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Domain 869..868

Domain 869..868

Domain 869..868

Domain 869..868

Domain 869..868

Domain 869..868

Domain 869..868

Domain 869..868

SQ Sequence 868 AA:  
 Query Match 93.9%; Score 4292.5; DB 18; Length 868;  
 Best Local Similarity 93.2%; Pred. No. 0;  
 Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

QY 1 MELVNIPLVHLITLVAASGTEKLPKAPVITPTLETDALVEEVAFMCAVESYPOPEIS 60  
 Db 1 melvniplvgmltlvalasgteklpkapvitptletvdalveevafmcavesypopels 60  
 QY 61 WTRNKILIKLFETRYISIRENGQLTILSVESDSDGICYCTANNGVGAESGALQVKK 120  
 Db 61 wtrnkililkfetryisirengqltilsvesdsgicyctannvggavesgalqvkk 120  
 QY 121 PKITPPINVKIIEGLKAVLPCTTMGNKPSYWKSGSPLENRNRIAVLEGSLRIHV 180  
 Db 121 pkitpplnvkiiegkavlpcttmgnkpsvwlksgsplernrnriavlegslrlhvv 180  
 QY 181 OKEDAGQYRCVAKNSLGTAYSKVVLLEFEVFAIRAPESHNVTFGSFVTLHCTAGIPV 240  
 Db 181 okedagqyrcvaknslgtayskvvllefevfarirapeshnvtfgsfvtlhtctagipv 240  
 QY 241 PTTIENGNAVSSGSIQESYKDRVIDSRLOLFTPKPGLYTICIAQNKGEKSTAKAAT 300  
 Db 241 pttiengnavssgsiqesykdrrvidsrloqlftpkpgltyticiaqnkgekstakaaat 300  
 QY 301 ISIAEMSKPQKNGCYCAOYREVCNAYLADALVFLWTSYADPEAOELVHTANELK 360  
 Db 301 isiaemskpqkngcycaoyrevcnayladalvflwtsyadpeaoelvhtanelk 360  
 QY 361 VVSPYCRPAEALCNHIFQECSPGVPTPIPCREYCLAVELCAKEMLMEKETHG 420  
 Db 361 vvspycrpaealcnhifqecspgvptpipcreyclavelcakemlmekeethg 420  
 QY 421 LYRSMHLISVPKCSKLPDSMHWDPACARLPDLVYKNEKLTFFPMTSSKSPVDIPNPS 480  
 Db 421 lyrsmhllisvpkcsklpdsmhwdpacarlpdlvyknekltpfpmstsskspvdipnps 480  
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 Db 481 ssssefsyptsmvtiisissfaiflittylccrrkqkknkresaaavltp 540  
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 Db 601 eptwvavkmlkeesasdmqadfqreaalmaefdpnntvklgvcagvapkmcclfeynav 660  
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 Db 660 gdineflrsmshphtvcslshsdlsrtravspgppplscaeqlclarqvaagmaylsertk 719  
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 QY 781 TESDVWAVGVVLMWEIFSYGLQPYTGMAHEEVIYVRDGNILSCPENCPVELYNMLRLCWS 840  
 Db 780 tesdvwavgvvlmwelfsyglqpytgmaheevlyyvrdsnllacpencpvelynmlrlcws 839  
 QY 841 KLPA DRPSTSHRIIRLIERMCEERAGTYSV 869  
 Db 840 klpadrpfstshrlirmceragetyv 868

## RESULT 7

AAW26507  
 AAW26507 standard; Protein: 868 AA.

AAW26507;

06-JAN-1998 (first entry)

Rat Dmk receptor.

Dmk receptor; tyrosine kinase receptor; signal transduction; assay; therapy; diagnosis.

Rattus sp.

Key Location/Qualifiers

Peptide 1..19

Domain 20..492

Domain 492..521

Domain 522..868

Domain 869..868

Domain 869..868

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 16, 2002, 13:36:00 ; Search time 37.92 Seconds

(without alignments)  
3964.467 Million cell updates/sec

Title: US-09-817-487a-2

Sequence: 1 MRLVNIPLVHILIVAFSG.....TSIRILIRKRCERAGIVSV 869

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 1000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP archaea  
2: SP bacteria  
3: SP fungi  
4: SP human  
5: SP invertebrate  
6: SP mammal  
7: SP mhc  
8: SP organelle  
9: SP phage  
10: SP plant  
11: SP rodent  
12: SP virus  
13: SP vertebrate  
14: SP unclassified  
15: SP virus  
16: SP bacteriophage  
17: SP archaea

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4558	99.8	869	4	015146
2	4292.5	93.9	869	1	062838
3	4269.5	93.4	868	11	061005
4	4220.5	92.4	860	11	061005
5	4136	90.5	871	11	061987
6	4128	90.3	881	11	061988
7	2897	63.4	946	13	007153
8	1602	35.1	354	13	09DDA2
9	1129.5	24.7	724	5	09V6K3
10	966.5	21.2	1145	5	09B6K8
11	802	17.6	821	13	09YH44
12	801	17.5	811	13	09YH43
13	792.5	17.3	839	4	075682
14	778	17.0	685	5	024488
15	773.5	16.9	928	5	09B1K1
16	772	16.9	902	5	017576

17	754.5	16.5	591	4	015656	015656 homo sapien
18	750.5	16.4	790	13	090699	090699 gallus gall
19	740.5	16.2	503	4	015655	015655 homo sapien
20	738.5	16.2	486	13	09P5T9	09P5T9 xenopus lae
21	724.5	15.9	802	13	042127	042127 xenopus lae
22	720	15.8	782	11	061563	061563 mus musculu
23	720	15.8	796	13	091287	091287 pleurodeles
24	720	15.8	972	5	026614	026614 strongyloce
25	715	15.6	800	4	090522	090522 homo sapien
26	712	15.6	800	4	090522	090522 homo sapien
27	709	15.6	800	13	091373	091373 xenopus tr
28	708	15.5	800	11	09JHX9	09JHX9 rattus norv
29	705.5	15.4	922	13	090413	090413 brachydanio
30	702.5	15.4	814	13	091897	091897 xenopus lae
31	697.5	15.3	802	6	09SM13	09SM13 bos taurus
32	686.5	15.2	650	11	063709	063709 rattus rat
33	685.5	15.2	800	13	09P5T9	09P5T9 xenopus lae
34	690.5	15.1	989	13	0918X3	0918X3 brachydanio
35	686.5	15.0	824	13	09P5T9	09P5T9 gallus gall
36	681	14.9	824	13	090749	090749 gallus gall
37	681	14.9	765	4	096KM2	096KM2 homo sapien
38	681	14.9	765	4	096KM1	096KM1 homo sapien
39	679	14.9	819	4	096KM0	096KM0 homo sapien
40	677	14.8	822	11	060818	060818 mus musculu
41	676	14.8	876	11	060752	060752 mus musculu
42	676	14.8	782	6	09TW23	09TW23 oryctolagus
43	671	14.7	806	13	090200	090200 brachydanio
44	670	14.7	609	13	091776	091776 xenopus lae
45	670	14.7	1362	13	09PV24	09PV24 xenopus lae

## ALIGNMENTS

RESULT 1

ID 015146 PRELIMINARY; PRT; 869 AA.

AC 015146;

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE MUSCLE SPECIFIC TYROSINE KINASE RECEPTOR.

GN MUSK.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-96009854; PubMed-7546737;

RA Valenzuela D.M., Stilt T.N., Distefano P.S., Rojas E., Mattsson K.,

RA Compton D.L., Nunez L., Park J.S., Stark J.L., Gies D.R., Thomas S.,

RA Lebeau M.M., Fernald A.A., Copeland N.G., Jenkins N.A., Burden S.J.,

RA Glass D.J., Yancopoulos G.D.;

RT "Receptor tyrosine kinase specific for the skeletal muscle lineage:

RT expression in embryonic muscle, at the neuromuscular junction, and

RT after injury."

RL Neuron 15:573-584(1995).

RN [2]

RP SEQUENCE FROM N.A.

RA Valenzuela D.M., Rojas E., Yancopoulos G.D.;

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF006464; AAB63044.1;

DR HSSP: P11362; IPKG.

DR InterPro: IPR002453; Beta\_tubulin.

DR InterPro: IPR000719; Euk\_Pkinase.

DR InterPro: IPR000024; Fz\_domain.

DR InterPro: IPR003598; Ig\_c2.

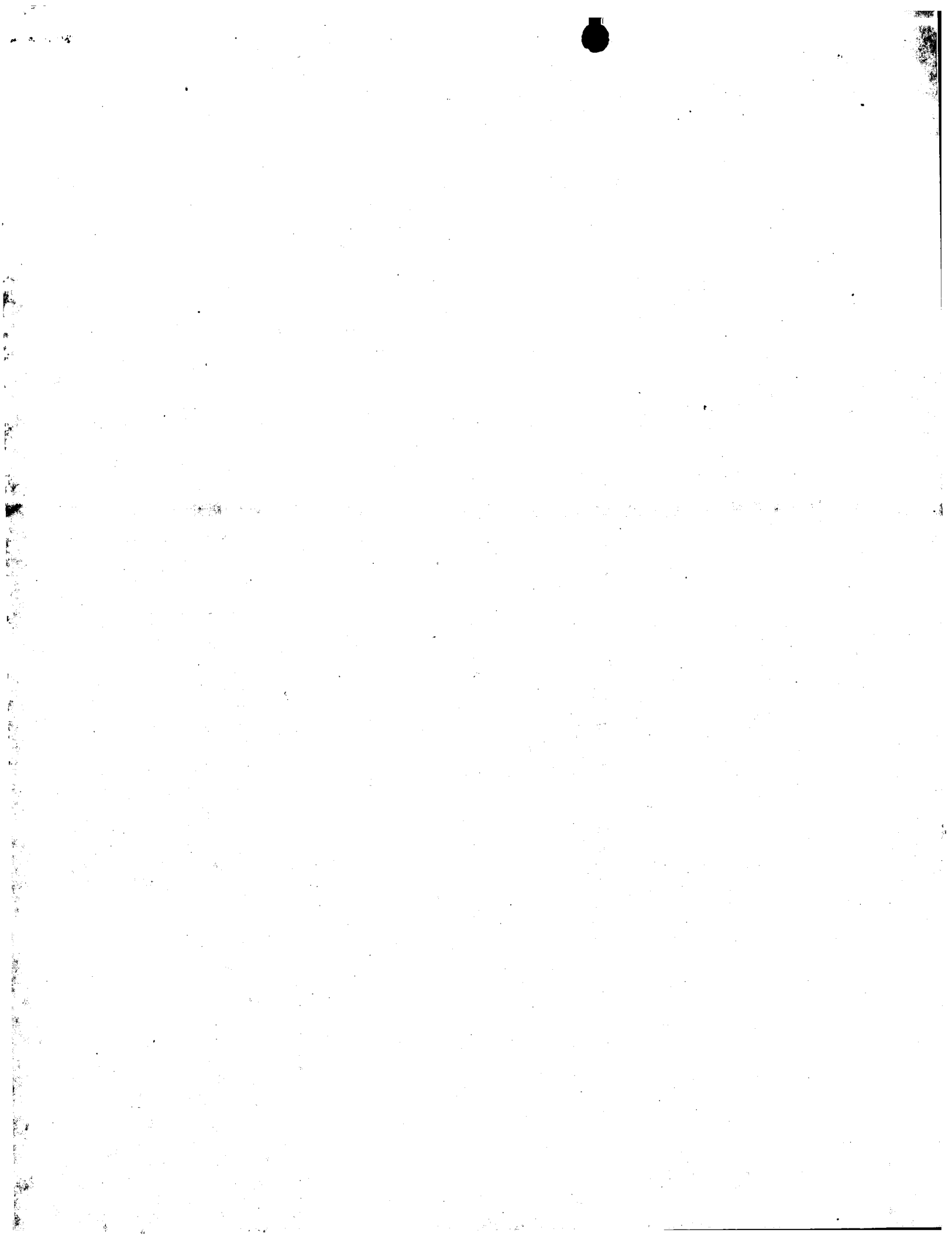
DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR001245; Tyr\_kinase.

DR Pfam: PF01392; Fz\_1.

DR Pfam: PF00047; Ig\_3.

DR Pfam: PF00069; pkinase; 1.



PRINTS: PRO0109; TYRKINASE.  
 DR SMART: SM00408; IGC2; 3.  
 DR SMART: SM00219; TYRK; 1.  
 DR PROSITE: PS50038; F2; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS00228; TUBULIN\_B\_AUTOREG; 1.  
 KW ATP-binding; Immunoglobulin domain; Kinase; Receptor; Transferase;  
 KW Tyrosine-protein kinase.  
 SQ SEQUENCE 869 AA; 97056 MW; 3DDC20E179FA010C CRC64;

Query Match 99.8%; Score 4558; DB 4; Length 869;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

1 MRELVINIPVHILTLVAFASTGTEKLPKAPVITTPLEVDALVEEVAIFMCAVESYPOPEIS 60
1 MRELVINIPVHILTLVAFASTGTEKLPKAPVITTPLEVDALVEEVAIFMCAVESYPOPEIS 60
61 MTRNKILIKLFTIRYSIRENGQLTILSVESDDGIYCCANNVGAVESGALQVKK 120
61 MTRNKILIKLFTIRYSIRENGQLTILSVESDDGIYCCANNVGAVESGALQVKK 120
121 PRTIRPINVKIIEGLKAVLPCTMGNPKPSVSWIKGSDPLRENSRIAVLESGLRIHNV 180
121 PRTIRPINVKIIEGLKAVLPCTMGNPKPSVSWIKGSDPLRENSRIAVLESGLRIHNV 180
181 OKEDAGQRCVAKNSLGTAYSKVVKLEFVFAIRILAPESHNVYTGSEFTLHCTATGIV 240
181 OKEDAGQRCVAKNSLGTAYSKVVKLEFVFAIRILAPESHNVYTGSEFTLHCTATGIV 240
181 OKEDAGQRCVAKNSLGTAYSKVVKLEFVFAIRILAPESHNVYTGSEFTLHCTATGIV 240
241 PRTIENGNAVSSGSIQSVKDRVIDSRLOFTIKPGLYTCIATNKHEKSTKAAT 300
241 PRTIENGNAVSSGSIQSVKDRVIDSRLOFTIKPGLYTCIATNKHEKSTKAAT 300
301 ISIAEMSKPKONKGYCAQYREGVNAVILAKALVFLNTYADPEAOELLVHTAMNELK 360
301 ISIAEMSKPKONKGYCAQYREGVNAVILAKALVFLNTYADPEAOELLVHTAMNELK 360
361 VVSPVCRPAEALCNHIFOECSPEVVPPIPIREYCAVAKELCAEMVMEKTRHG 420
361 VVSPVCRPAEALCNHIFOECSPEVVPPIPIREYCAVAKELCAEMVMEKTRHG 420
421 LYRSEMHLLSVPKOSKLSHMHDPACARLPHLDYKNENLTPPMTSSKPSVDIPNLS 480
421 LYRSEMHLLSVPKOSKLSHMHDPACARLPHLDYKNENLTPPMTSSKPSVDIPNLS 480
481 SSSSFVSPTYSMTVIISISSFAIFLITLITLCCRRKKONKRESAAVTLTLP 540
481 SSSSFVSPTYSMTVIISISSFAIFLITLITLCCRRKKONKRESAAVTLTLP 540
541 SELLDLHLHPNPMQRPMLLPKLSLEYPRNNIEYRDGEGAFGRVFOARAPGLLP 600
541 SELLDLHLHPNPMQRPMLLPKLSLEYPRNNIEYRDGEGAFGRVFOARAPGLLP 600
601 EPTTNAVVKLKEASADMDQADFOREALAELAEFNPNIYKLGVCAGKPKCLLFEYMA 660
601 EPTTNAVVKLKEASADMDQADFOREALAELAEFNPNIYKLGVCAGKPKCLLFEYMA 660
661 GDNIEFLRSMPTVCSLSHSDLSMAQVSSPGPPPLSCAEOICIAQVAAAGAAVYSERK 720
661 GDNIEFLRSMPTVCSLSHSDLSMAQVSSPGPPPLSCAEOICIAQVAAAGAAVYSERK 720
721 FVHRDLATRCVLENNVYKIDFGLSRNIYSADYKANKENDAIPIRMPPEISIFNRYT 780
721 FVHRDLATRCVLENNVYKIDFGLSRNIYSADYKANKENDAIPIRMPPEISIFNRYT 780
781 TESDVAAVGVLMETISYGLQPYGMAHEVITYYVDGNTLSPENCPELYNMLRLCS 840
781 TESDVAAVGVLMETISYGLQPYGMAHEVITYYVDGNTLSPENCPELYNMLRLCS 840

```

QY 841 KLPADRPSTIRILERMCEAGETVSV 869  
 DB 841 KLPADRPSTIRILERMCEAGETVSV 869

RESULT 2  
 ID 062838 PRELIMINARY; PRT: 868 AA.  
 AC 062838;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DE MOLECULE-SPECIFIC TYROSINE KINASE RECEPTOR MUSK.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC NCBI-TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96009854; PubMed=7546737;  
 RA Valenzuela D.M., Stitt T.N., Stefano P.S., Rojas E., Mattsson K.,  
 RA Compton D.L., Nunez L., Park J.S., Stark J.L., Gies D.R., Thomas S.,  
 RA LeBeau M.M., Bernad A.A., Copeland N.G., Jenkins N.A., Burden S.J.,  
 RA Glass D.J., Yancopoulos G.D.;  
 RT "Receptor tyrosine kinase specific for the skeletal muscle lineage:  
 RT expression in embryonic muscle, at the neuromuscular junction, and  
 RT after injury.";  
 RL Neuron 15:573-584 (1995).  
 CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC EMBL: U34985; AAA0956.1; -  
 DR HSSP: P13362; IIGK.  
 DR InterPro: IPR002453; beta\_tubulin.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR003598; F2\_domain.  
 DR InterPro: IPR003066; Ig\_MHC.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF01392; F2; 1.  
 DR Pfam: PF00047; Ig; 3.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PRO0109; TYRKINASE.  
 DR SMART: SM00408; IGC2; 3.  
 DR SMART: SM00219; TYRK; 1.  
 DR PROSITE: PS50038; F2; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS00228; TUBULIN\_B\_AUTOREG; 1.  
 KW ATP-binding; Immunoglobulin domain; Kinase; Receptor;  
 KW Serine/threonine-protein kinase; Transferase;  
 SQ SEQUENCE 868 AA; 96821 MW; C146B4E74EE25B24 CRC64;

Query Match 93.9%; Score 4292.5; DB 1; Length 868;  
 Best Local Similarity 93.2%; Pred. No. 0;  
 Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

```

1 MRELVINIPVHILTLVAFASTGTEKLPKAPVITTPLEVDALVEEVAIFMCAVESYPOPEIS 60
1 MRELVINIPVHILTLVAFASTGTEKLPKAPVITTPLEVDALVEEVAIFMCAVESYPOPEIS 60
61 MTRNKILIKLFTIRYSIRENGQLTILSVESDDGIYCCANNVGAVESGALQVKK 120
61 MTRNKILIKLFTIRYSIRENGQLTILSVESDDGIYCCANNVGAVESGALQVKK 120
121 PRTIRPINVKIIEGLKAVLPCTMGNPKPSVSWIKGSDPLRENSRIAVLESGLRIHNV 180
121 PRTIRPINVKIIEGLKAVLPCTMGNPKPSVSWIKGSDPLRENSRIAVLESGLRIHNV 180
181 OKEDAGQRCVAKNSLGTAYSKVVKLEFVFAIRILAPESHNVYTGSEFTLHCTATGIV 240
181 OKEDAGQRCVAKNSLGTAYSKVVKLEFVFAIRILAPESHNVYTGSEFTLHCTATGIV 240

```





CC method uses a mutated PKR nucleic acid which comprises a modification  
CC to the intracellular and extracellular domains, or comprises a  
CC modification to the intracellular domain and excludes any nerve growth  
CC factor receptor(s) (NGF). The method uses mutated PKR as a cell  
CC surface marker, and is useful for identifying genetically modified cells,  
CC especially immunoselection of transduced mammalian cells, and for  
CC identifying mammalian cells expressing a protein of interest. The  
CC genetically modified marked cells may be used in an autologous or  
CC allogeneic setting e.g. gene therapy for bone marrow transplants, graft  
CC facilitation or immune reconstitution.

XX Sequence 869 AA:

Query Match 100.0%; Score 4569; DB 22; Length 869;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 869; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Y 1 MRELVNIPLVHILTVAFSGTEKLPKAPVITTPLETVDAIVEAVTFMCAVESYPOPEIS 60  
Db 1 mrelvnlplvhlitvafsgteklpkapvlttpletvdaiveavtfmcavesypqpeis 60  
Qy 61 WTRNKILIKLFDTRYISIRENGQLTILSVESDDGIYCTANNVGAVESGALQVKNK 120  
Db 61 wtrnkililkfdtryisirengqltllsvedsddgiyctannvgavescgalqvknk 120  
Qy 121 PKTRPPINVKIIEGKAVLPCTTGNPKPSYWKGDSPLENSRIANLESGSRIRHNV 180  
Db 121 pktrppinvkiliegkavlpccttgnpkpsywkgdsplemnriavlesgsrlrhnv 180  
Qy 181 OKEDAGYRCVAKNSLGTAYSKVKEEFEPARILRAPESHNVTFGSFVTLHCTATGIPV 240  
Db 181 qkedaggyrcvaknslgtayskvkleefeparilrapeshnvtfgsfvtlhtctatgipv 240  
Qy 241 PRTIENGNAVSSGISEQSVKDRVIDSRLOLFTKPGILYICATFNKHEKSTAKAAT 300  
Db 241 prtiengnavssgiseseqvdrvidsrloqlftkpgilyicatfnkhekstakaat 300  
Qy 301 ISIAEMSKPOKNGKYCAQYRGECVNAVIAKDALVPLNLSVADPREAOELLYHTAMNEIK 360  
Db 301 isiaemskpokngkycaqyrgecvnaviakdalvplnlsvadpreaoellyhtamneik 360  
Qy 361 VVSPVCPRAAEALCNHIFQECSPGVPTPIPCREYCLAVELFCAKEMLVMEETKARG 420  
Db 361 vvspvcpraaealcnhifqecspgvptpircreyclavelfcakemlvmeekthrg 420  
Qy 421 LYRSMHLISVPCCKSLPSMMDPTACARLPHLDYNKENLKTFFPMTSSKPSVDIPNLS 480  
Db 421 lyrsmhlisvpcckslpsmmdptacarlp hldynkenlktffpmtsskpsvdipnls 480  
Qy 481 SSSSFSYPTYSMTVIISIMSFVILTTTLYCCRRROMNKKRESAAVLTMLTP 540  
Db 481 ssssfysptysmvtviisimsfviltttlyccrrromnkkresaaavltmltp 540  
Qy 541 SELLDRLHPNPMYOMRPLLNLKLSLEYPRNNIEYVDIGEGAFGRFQARAPGLPY 600  
Db 541 sellldrlhpnpmymrpll nllklsleyprnnieyvdigegafgrfqrarapglpy 600  
Qy 601 EPTFVAVAKMLKEASADMOADFORBALMAEPDNPNTYKLLGVCAVKGKMLFEYMAV 660  
Db 601 eptfvavakmlkeasadmoadforbalmaepdnpntykllgvcavgkmlfeymav 660  
Qy 661 GDNLNFKLSMSPHTYCSISHSOLSMRAOVSSPGPPLSCABOLICARQVAAAMATLSERK 720  
Db 661 gdlnlnfklsmsphtycsishsolsmraovsspgpplscabolicarqvaaamatlserk 720  
Qy 721 FVHRDLATRNCLVGENMYVKIADFGISRNISADYYKANKENDAIPIRWMPESISYNYRT 780  
Db 721 fvhrdlatrnclvgenmyvkiadfgisrnisadykankendaipirwmpesisyntyrt 780  
Qy 781 TESDVMAAGVYLMEFSGLOPYGMAHEVLYYRDGNIISCPENCPEVELYNLRCLWS 840  
Db 781 tesdvmaagvylmefsglopygmahevlyyrdgniiscpencpevelynlrclws 840

Qy 841 KLPADEPSTSIHRIIERMERCERAGTSVY 869  
Db 841 klpadrpsstsihriiermerceraegtvsy 869

RESULT 3  
ID. AAM26611 standard; Protein: 869 AA.

AC AAM26611;  
DE 27-JAN-1998 (first entry)

DE Human muscle-specific kinase (Musk).  
KW Receptor tyrosine kinase; muscle specific kinase; Musk; Dmk; human.  
KW ligand; agrin; diagnosis; therapy.

OS Homo sapiens.  
PN WO9721811-A2.

PD 19-JUN-1997.  
PF 13-DEC-1996; 96WO-US20696.

PR 10-MAY-1996; 96US-0644271.  
PR 15-DEC-1995; 95US-0008657.

PA (REGE-) REGENERON PHARM INC.  
PI Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD;

DR WPI: 1997-332783/30.  
DX N-PSDB; AAT90473.  
PT Nucleotide sequences encoding human agrin and muscle specific kinase  
PT and related receptor - used in diagnosis and treatment of disorder  
PT with muscle atrophy

PS Example 4; Fig 4; 120pp; English.

CC This polypeptide comprise a novel human receptor tyrosine kinase  
CC designated muscle specific kinase (Musk) that is expressed in  
CC normal and denervated muscle. Musk is alternatively referred to  
CC Dmk for denervated muscle kinase. The amino acid sequence was  
CC deduced from an isolated cDNA clone (see AAT90471). Rat Musk (see  
CC AAM26610) has also been identified. Use of Musk to generate anti-  
CC Musk antibodies and in the diagnosis of neurological or other  
CC disorders is disclosed. Assay systems that may be used to detect  
CC and/or measure ligands that bind the musk gene product are provided.  
CC A claimed method of promoting the growth, differentiation or  
CC survival of Musk receptor-expressing cells involves administration  
CC to the cell of agrin (see AAM26609). Such cells include muscle,  
CC heart, spleen, ovary and retina cells, or cells genetically  
CC engineered to express the Musk receptor.

XX Sequence 869 AA:

Query Match 99.8%; Score 4558; DB 18; Length 869;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 867; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRELVNIPLVHILTVAFSGTEKLPKAPVITTPLETVDAIVEAVTFMCAVESYPOPEIS 60  
Db 1 mrelvnlplvhlitvafsgteklpkapvlttpletvdaiveavtfmcavesypqpeis 60  
Qy 61 WTRNKILIKLFDTRYISIRENGQLTILSVESDDGIYCTANNVGAVESGALQVKNK 120  
Db 61 wtrnkililkfdtryisirengqltllsvedsddgiyctannvgavescgalqvknk 120



Qy	121	PRITRPPINWVITIBELKAVLCTMTMPKPKSVSMIKDSDPLREMSRIATVESSSLRHHV	180
Dp	121	Pkltprplnvnklldeglkavtrpcttmgnpkrpsvswikdspdrlrensrtaivlaessgslilnhv	180
Qy	181	OKEDAGQYRCVAKNSLSLGAYSKVYKLEFEFEYARILRARESHNNTFGSFFVYLHCTAGIPV	240
Dp	181	qkedagqyrcvakhnsldgatakvkklevevfarlilrpeshnntfgsfvllhctagipv	240
Qy	241	PTTIWENGNAVSSGSIODESVKDRVIDSRLOLFTFKPGLTYCTATNKHGEKSTAKAAAT	300
Dp	241	ptltwengnavssgslqdesvkdvdvrsrlqlftfkpglyctatnkhgkfstakaaat	300
Qy	301	ISIAEWSRPOKDNNGYCAQYQYRGVCNNAVLKADALVFNSTYSAPDEEAOELLVTANNEIK	360
Dp	301	isliewsrpqgdanngycaqyqyrgvcnavlakdavlfnstysadpeeagellvhtananneik	360
Qy	361	VVSPYCRPAALALCNHIFOCSPGAVPTPIICREYLCVKEFCFCAKEVLVNEEKTHNG	420
Dp	361	vvsprcpraeaalcnhlfgecspgvvptribrcrcyglcvkefckekvlvneekthng	420
Qy	421	LYRSEBHLISVPKCSKULPSMHWDPFACARLPHLDYKNENLKTREPMPTSRSKPYDINLES	480
Dp	421	lyrsemhlisvpecsklpsmhwpdtacarlphldynkenlktfpmptsrskpydvdipls	480
Qy	481	SSSSFSFSPYMTVTIISMSRAIFVLTITTLVCCRKKOKMKNKRESAAVLTTLTP	540
Dp	481	ssssfsfspymtvtiismsraifvlltlttlvccrrkvmknkresaaavlttltp	540
Qy	541	SELLDLRLHPNMTQRPRLNPLRLLEKLEYPNNIEVVRDIGEGAGRYVQAAPLLTY	600
Dp	541	sellldrlhprnmqrpmllnpklrlleypnnleavyridgsagafgyrfdqatapgllty	600
Qy	601	EPFTWAVAKMLKEBASADMQADFOREALMAEFDPNIVKLELVCAGVGRFMCILFEYMAV	660
Dp	601	epftmwavakmlkeesaadmqadfgrealaefdpnplvklvgcavgyrkmcllfeymav	660
Qy	661	GDWLEPLRSMRPHVYCSLSHSDLSMRQVSSRPPRPPLCSAEOLCIRQVAAAGNAVISEK	720
Dp	661	gdwleflrsmrphvcslshsdlsmrqvaspprpplcsaeqcliarqvaagnavisek	720
Qy	721	FVHRDLATRNCLVGENNVAVKIADFGLSRNTYSADYVYKANNDNIPIRMPMPESIEFNRAT	780
Dp	721	fvhrdlatrnclovgenmvkiadfglsrnltyasadyykanendiprlrmppeesifnryc	780
Qy	781	TESOVNAVGVWLMEISYGLQPYGYMAHEEVIYVRDGNILSCPENCPELVYLMRLCS	840
Dp	781	tesovnavgvwlmeifayglpygymaheeviyvrdgnllscpencpeelylmrlcws	840
Qy	841	KLPRDRSPFSIHRLIRNCRERAGCTSV	869
Dp	841	kllprdrpsfshrlirncrereagctsv	869

XX 21-JUL-1993; 93US-0095658.  
 PF  
 XX  
 PR 19-JAN-1995; 95US-0374834.  
 PR 21-JUL-1993; 93US-0095658.  
 XX  
 PA (REG-); REGENERON PHARM INC.  
 XX  
 P1 Rojas EA, Valenzuela DM;  
 XX  
 DR WPI; 1997-414593/38.  
 DR N-PSDB; AAT87073.  
 XX  
 PT New isolated human denervated muscle kinase receptor - used to  
 PT develop products for the diagnosis and treatment of neurological,  
 PT muscle or neuromuscular disorders  
 XX  
 PS Claim 4; Column 31-36; 31pp; English.  
 XX

CC This polypeptide comprises the human Dmk receptor (AA026506), a novel  
CC tyrosine kinase receptor that is expressed in high levels in  
CC denervated muscle. Its amino acid sequence was deduced from an  
CC isolated nucleic acid molecule (see AA087073). The Dmk receptor can  
CC be used to screen for agents that interact with Dmk. Agents that  
CC bind to the receptor may mediate survival and differentiation in  
CC cells naturally expressing the receptor, but may also confer survival  
CC and proliferation when used to treat cells engineered to express the  
CC receptor. Dmk receptor polypeptides and polynucleotides can also be  
CC used for detecting aberrancies in the function or expression of the  
CC receptor which may be used in the diagnosis of muscular or other  
CC disorders. Manipulation of the receptor or agonists which bind this  
CC receptor may be used to treat neurological diseases, diseases of  
CC muscle or neuromuscular unit disorders, including Alzheimer's  
CC disease, Parkinson's disease, amyotrophic lateral sclerosis (Lou  
CC Gehrig's disease), idiopathic torsion dystonia and muscle atrophy.  
CC The extracellular domain (ECD) of the receptor can be used to block  
CC the binding of receptor to target cells. A receptorbody comprising  
CC the ECD fused to a human Ig gamma-1 constant region is claimed.

**SQ Sequence 869 AA;**

Query Match	99.8%	Score 4558;	DB 18;	Length 869;
Best Local Similarity	99.8%	Pred. NO. 0;		
Matches 867; Conservative	1;	Mismatches	1;	Indels 0; Gaps 0

QY	1	MRELVPNPLVHIIITLVAFSGTEKPKAPVITTPLEETVDALVEEVATMCAVESTYPOBEIS	60
Db	1	mtelvnplvhllelvafsgtekpkapvittlprietdalaiveeatmcaesypgeis	60
QY	61	WTRAKIIILKLEDPYSTRRENGQIIITLISVEDSDGICCTANNVGGAVSCGALQYMK	120
Db	61	wtrklliklfdctylstrngqlltlisvedsdgilycctannvggavscgalyqmk	120
QY	121	PKITRPPINVKIIEGLKAVLPCTTMGNPKPSVWIKSDSEPLRENSRIAYVESGSLRIHNV	180
Db	121	pkitrrppinvkliegkavlpcttmgnpkpsvwiksdseplrensrilayvesgslrihnv	180
QY	181	QKEDAGQYRCARKNSLSTATSKSVYKLEFVFAIRLRAPDESHNTFSGFTVLHCTATGIPV	240
Db	181	qkedagqyrcarknslstayskvkclevefaiirrpeshnvtfsgfvtlhcatacgv	240
QY	241	PTIMIENGNNVSSGSIOESYKXDEVIDSROLFTRKGLTTCIATNKHGEKSPAKAAAT	3000
Db	241	ptimienngnavssgsiqesvktadvidsrqlftrkpglytclatnkhgefstakaaat	3000
QY	301	ISIAEWSKPOKDNKGKYCAQYRGEVCANVLAARDALVFNLTSYADPEEAQELLVHTANWELK	3600
Db	301	islaewskpqdkngkycaqyrgvcanvalakdalfvntsyadpeeaqellvhtanwelk	3600
QY	361	VVSPVCGPAAEALICNHIPOBDSGGVPTPIPICREKCLAVKELFCACKELVNEERTKTHG	4200
Db	361	vvspvcgpaaeallicnhlipoecpvgvptpircrcavkelfckekvlnveektthrg	4200



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OY 421 LYSEHLLSVKPSKSLPSMMDPTACARLPHLDYKNENKTPPMTSKSPVDIPNLP 480
XX |||||
DB 421 lysemhllsvpecsklpsmhwdptacarilphldynkenktprmtsskspvdipnlp 480
OY 481 SSSSFVSPTYSMTVIISMSFAIFVLLITTLVCCRKKQWKNKKRESAAVLTTLTP 540
XX |||||
DB 481 ssssfvsptysmtvliismsfaifvllitlttlvccrrkkqwnkkresaaavltiltp 540
OY 541 SELLDRLHPNPMYQRMPLLNPKLSLEPRNNIEYVDIGSGAGRVFOARAPGLLPY 600
XX |||||
DB 541 sellldrlhpnpmymqrmpllnpkllsleprnnieyvdi gsgagr vfoarapgl lpy 600
OY 601 EPTTVAVKMLKEEASADMOADFOREALMAEFNDPNIVKLLGCACVGRPMCLIFEYMA 660
XX |||||
DB 601 epttvaavkmlkeesaadmqadfgreaalmaefndpnivkllgvcavgrpmcllfeymay 660
OY 661 GDLNERTSMSPHTVCSLSHSDLSMAQVSSPEPPPLSCADJICARQVAAAGVAYISERK 720
XX |||||
DB 661 gdlneftrsmshpvtcs lshsdlsmaq vsspeppplscad jicarqv aaagvay iserk 720
OY 721 FVHRDLATRNCLVGENMVKIADFGLSRNIYSADYKKNENDAPIRMMPESEIENRYT 780
XX |||||
DB 721 fvhrdlatrnclvgenmvvk iadfglsrniysadykknendaip rmmpe seienryt 780
OY 781 TESDVAVGVVIMETFSYCLQPYGMAHEEVIYVRDGNILCPENCPELYNLMLCWS 840
XX |||||
DB 781 tesdvavgvvime tfsyclqpy gmaheevi yvr dgnilc pency nlm l cws 840
OY 841 KLPADRPSTSIHRITERMCCERAEQTVSV 869
XX |||||
DB 841 klpadrpstsihr itermccer aeqtvsv 869

RESULT 5
AAW26610
ID AAW26610 standard; Protein: 868 AA.
XX
AC AAW26610;
XX
DT 27-JAN-1998 (first entry)
XX
DE Rat muscle-specific kinase (Musk).
XX
KW Receptor tyrosine kinase; muscle specific kinase; Musk; Dmk; rat;
KW ligand; agrin; diagnosis; therapy.
XX
OS Rattus sp.
XX
FH Key location/Qualifiers
FH Peptide 1..19
FT /Label- S1g_peptide
FT Domain 21..492
FT /Label- Extracellular_domain
FT Domain 493..521
FT /Label- Transmembrane_domain
FT Domain 522..868
FT /Label- Intracellular_domain
XX
PN W09721811-A2.
XX
PD 19-JUN-1997.
XX
PE 13-DEC-1996; 96WO-US20696.
XX
PR 10-MAY-1996; 96US-0644271.
PR 15-DEC-1995; 95US-0008657.
XX
PA (REGC-) REGENERON PHARM INC.
XX
PI Bowen DC, Glass DJ, Valenzuela DM, Yancopoulos GD;
XX WPI: 1997-332783/30.

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DR N-PSDB: AAT90472.
XX Nucleotide sequences encoding human agrin and muscle specific kinase
PT and related receptor - used in diagnosis and treatment of disorder
PT with muscle atrophy
XX
PS Example 1; Fig 1; 120pp; English.
XX
CC This polypeptide comprise a novel rat receptor tyrosine kinase
CC designated muscle specific kinase (Musk) that is expressed in
CC normal and denervated muscle. Musk is alternatively referred to
CC Dmk for denervated muscle kinase. The amino acid sequence was
CC deduced from an isolated cDNA clone (see AAT90472). Human Musk (see
CC AAW26611) has also been identified. Use of Musk to generate anti-
CC Musk antibodies and in the diagnosis of neurological or other
CC disorders is disclosed. Assay systems that may be used to detect
CC and/or measure ligands that bind the musk gene product are provided.
CC A claimed method of promoting the growth, differentiation or
CC survival of Musk receptor-expressing cells involves administration
CC to the cell of agrin (see AAW26605). Such cells include muscle,
CC heart, spleen, ovary and retina cells, or cells genetically
CC engineered to express the Musk receptor.
XX
SQ Sequence 868 AA:
Query Match 93.9%; Score 4292.5; DB 18; Length 868;
Beat Local Similarity 93.2%; Fred. No. 0;
Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;
OY 1 MRELVINPLVHLITLVAESGTEKLPKAPYITPLEVDALVEEATFMCAVESYPOPEIS 60
DB 1 mrelvniplqlmlltvalafsgtek lpkapyitplevdalveeatfmcavesypopeis 60
OY 61 WTRNKILIKLPTRSIRENGOLITLTVESDDGIYCCCTANNGVAGVSCGALQVKKK 120
DB 61 wtrnkililk lpt rsi rengol itl tve sddgi ycc ctanngv agvscgal qvkkk 120
OY 121 PKITRPINVKIIEGKAVLPCTTGNRPSPSWIKGDSPLRENSRIANLESGSLRIHNV 180
DB 121 pkitrpinvkiie gkavlpct tgnrpspsw ikgdspl rensri anle sgslri hnv 180
OY 181 OKEDAGQYRCVAKNSLGTAYSKVVKLEFEVFAIRIRAPESHNVTCGSFYTLLICTATGIPV 240
DB 181 okedagqyrcv aknslgtays kvvkl efevfa irirap eshnv t cgsfyt ll ictatg ipv 240
OY 241 PRTIENGNAVSSGSIOESVKDRVIDSRLOLFTIRPGLYCIATNKGKFSKAKAAT 300
DB 241 prtien gnavss gsi oesv kdrvid srlo lftirp glyci atnkgk fskakaat 300
OY 301 ISIAEMSKPOKDNKGYCAQYRGECNAVLAKDALVFIMTSYADDEACELLYHTAMNEX 360
DB 301 isiaemskp okdnkgyca qyrg ecnavl akdalvf imtsy addeac ellyht amn ex 360
OY 361 VSLAEWSKSGKESKYCGYRGVCDVALVKDVLFINTSYDPDEAGELLHTAMNEX 360
DB 361 vslae wsksg kesky cgyrg vcdval vkdv lfin tsy dpea gellht amn ex 360
OY 361 VVSPVCRPAEALLCNHIFDECSPGVPTPIPICREYCLAVNELPCANEMVMEKRTNG 420
DB 361 vvspvcrp aeallcn hifde cspgvpt pi picreycl avnelpc anemv mekrtng 420
OY 421 LYSEHLLSVKPSKSLPSMMDPTACARLPHLDYKNENKTPPMTSKSPVDIPNLP 480
DB 421 lysemhllsvpecsklpsmhwdptacarilphldynkenktprmtsskspvdipnlp- 479
OY 481 SSSSFVSPTYSMTVIISMSFAIFVLLITTLVCCRKKQWKNKKRESAAVLTTLTP 540
DB 481 ssssfvsptysmtvliismsfaifvllitlttlvccrrkkqwnkkresaaavltiltp 539
OY 541 SELLDRLHPNPMYQRMPLLNPKLSLEPRNNIEYVDIGSGAGRVFOARAPGLLPY 600
DB 540 sellldrlhpnpmymqrmpllnpkllsleprnnieyvdi gsgagr vfoarapgl lpy 599
OY 601 EPTTVAVKMLKEEASADMOADFOREALMAEFNDPNIVKLLGCACVGRPMCLIFEYMA 660
DB 600 epttvaavkmlkeesaadmqadfgreaalmaefndpnivkllgvcavgrpmcllfeymay 659

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QY 661 GDLNEFLRSMSPHTVCSLSHSDLSMRAQVSSPPPELSCAEOLCIARQVAGMAYLSERK 720
Db 660 gdlneflrsmshphtvcslshsdlsrtravspppplscaeqlclarqvaagmaylserk 719
QY 721 FVHRDLATRNCLVGENNVKVIADFGISRNITYSADYKKAENDAIPIRKMPPESTIFYNRYT 780
Db 720 fvhrrdlatrncclvgenmvvkiadfgisrnlisadykkaendaipirmppestifynryt 779
QY 781 TESDVAVAGVVLMEIFSYGLOPYYGMAHEEVIYVVDGNILSCPEKCPVELYNLMRLCMS 840
Db 780 tesdvavagvvlmeifsyglpyygmaheevlyyvrddgnllscpencilynlmrlcms 839
QY 841 KLPADRPSTSHRILERMCEAEGTVSV 869
Db 840 klpadrpstshrllqrmceragelgvv 868

```

## RESULT 6

AAW26507  
ID AAW26507 standard; Protein: 868 AA.

AC AAW26507;

06-JAN-1998 (first entry)

Rat Dmk receptor.

Dmk receptor; tyrosine kinase receptor; signal transduction; assay;

therapy; diagnosis.

Rattus sp.

Key Location/Qualifiers  
Peptide 1..19

FT Domain /Label- Sig.peptide

FT Domain /Label- Extracellular

FT Domain /Label- Transmembrane

FT Domain /Label- Intracellular

US5656473-A.

12-AUG-1997.

21-JUL-1993; 93US-0095658.

19-JAN-1995; 95US-0374834.

21-JUL-1993; 93US-0095658.

(REGG-) REGENERON PHARM INC.

Rojas EA, Valenzuela DM;

WPI; 1997-414593/38.

N-PSDB; AAT87074.

New isolated human denervated muscle kinase receptor - used to develop products for the diagnosis and treatment of neurological, muscle or neuromuscular disorders

Example 1; Column 19-24; 31pp; English.

This polypeptide sequence comprises the rat Dmk receptor, a novel tyrosine kinase receptor that is expressed at high levels in denervated muscle. Its amino acid sequence was deduced from an isolated cDNA clone (see AAT87074). Human Dmk receptor (see AAW26506) has also been identified and can be used to develop products for the diagnosis and treatment of neurological, muscle or neuromuscular disorders.

SQ Sequence 868 AA:

Query Match 93.9%; Score 4292.5; DB 18; Length 868;

Best Local Similarity 93.2%; Pred. No. 0;

Matches 810; Conservative 31; Mismatches 27; Indels 1; Gaps 1;

```

QY 1 MRELNIPLVHLTLVAASGTEKLPKAVITTPLETVDALEEVATFMCANESYPOPEIS 60
Db 1 mrelniplvhlmtlvaalsgtekpkavittpletvdaaleevatfmcavesypqpeis 60
QY 61 WTRNKILKLFDTYSIRENGLTLTISVEDSDGICYCTANNGVAGVSGALQVYMK 120
Db 61 wtrnkilklfdtrysirengltltisvedsdgicyctanngvagvescgalqvymk 120
QY 121 PKITRPPIVNVKIIIEGLKAVLPCTTGNPKPSVSWIKGSDPLRENSRIAVLESGLRIHNV 180
Db 121 pkitrppinvkiiiegkavlpcttgnpkpsvswikgsdplrensrilavlesgslrihmv 180
QY 181 QKEDAGYRCVAKNSLGRVYKLVKLEFEVFARILRARESHNVTGSGVTLHCTATGIPV 240
Db 181 qkedagyrvcaknslgrvykvlvklefevfarrilrarenshnvtgsgvvtlhcrtatgipv 240
QY 241 PTIWIENGNAVSSGSIQESYKDRYIDSRLOLFTTKPGLYCIATNKGKFKSTAKAAT 300
Db 241 ptlwiengnavssgsiqesykdrdyidsrloelftkpglyciatnkgkfkstakaat 300
QY 301 ISIAEKSPKQDNKGICYCAOYRGEVCNAVLAQDALVFLNTSYADPEAQLLVHTAMNBLK 360
Db 301 isiaekspkqdnkgicycaoyrgevcnavlaqdalvflntsyadpeaqllvhtamnblk 360
QY 361 VSPFCRPAEALCNHIFQCSPGVYPTPIRICEVLAKEFLCKEMLYMEKTRHG 420
Db 361 vspfcrpaecalcnhifqcspgvyptpiricevlakeflckemlymektrhg 420
QY 421 LYRSEMHLLSVKCSKLPSMHMDPTACARLPHLDYKNENLTFFPMTSKRSYDIPNLS 480
Db 421 lyrsfmhllsvkcsklpsmhmdptacarlp hldyknentlffpmtskrsyvipnls 480
QY 481 SSSSFVSPTSMVTYIISTMSFAIFVLTTITLYCCRRKKKKKRESAAVTLTLP 540
Db 481 ssssfvsptsmvtiyiistmsfaifvlttitlyccrrkkkkkresaaavtltlp 540
QY 541 SELLDRLHPNRYQRMPLLNPKLSLEYPRNIEYVRDIEGAFGRVQARAGILPY 600
Db 540 seldldrlhpnryqrmpllnpklsleyprnieyvrdiegafgrvqaragilpy 600
QY 601 EPTMVAVKMLKEBASADQADFORERALMAEFDNPIVRLGVCAVGKPCQLFEYMAV 660
Db 600 eptmvaavkmlkebasadmqadfgreaalmafndpni vrlgvavgkpcqlfeymay 659
QY 661 GDLNEFLRSMSPHTVCSLSHSDLSMRAQVSSPPPELSCAEOLCIARQVAGMAYLSERK 720
Db 660 gdlneflrsmshphtvcslshsdlsrtravspppplscaeqlclarqvaagmaylserk 719
QY 721 FVHRDLATRNCLVGENNVKVIADFGISRNITYSADYKKAENDAIPIRKMPPESTIFYNRYT 780
Db 720 fvhrrdlatrncclvgenmvvkiadfgisrnlisadykkaendaipirmppestifynryt 779
QY 781 TESDVAVAGVVLMEIFSYGLOPYYGMAHEEVIYVVDGNILSCPEKCPVELYNLMRLCMS 840
Db 780 tesdvavagvvlmeifsyglpyygmaheevlyyvrddgnllscpencilynlmrlcms 839
QY 841 KLPADRPSTSHRILERMCEAEGTVSV 869
Db 840 klpadrpstshrllqrmceragelgvv 868

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## RESULT 7

AAW2717  
ID AAR2717 standard; Protein: 868 AA.

AC AAR2717;

